

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 119902

TO: Phuong N Huynh

Location: 3d75 (3c70

Saturday, April 24, 2004

Art Unit: 1644 Phone: 272-0846

Serial Number: 10 / 005907

From: Jan Delaval

Location: Biotech-Chem Library

Rem 1A51

Phone: 272-2504

jan.delaval@uspto.gov

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                                                                                                                                                                    /tissue type="cerebellum"
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/note="unnamed protein product"
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Homo sapiens (human)
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Direct Submission

Direct Submission

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0018, Jahan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975) Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Bconomy, Trade and Industry of Japan; CDNA full Ansert sequencing:

Research Association for Biotechnology (RAB); CDNA library

CONSTRUCTION: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass Sequencing: RAB;

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing; HRI and

RAB; annotation: HRI and RAB.
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
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DNA linear HTG 23-SEP-2000 RP11-115C4, WORKING DRAFT SEQUENCE, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 141268) Waterston,R.H.

source

FEATURES

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COMMENT

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(bases 1 to 185467)
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Direct Submission Submitted (29-UU-2000) Genome Sequencing Center, Washington Submitted (29-UU-2000) Genome Sequencing Center, Washington Wo 63108, USA Washins sequence version replaced gi:9838075.
                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig3"
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64946. .67606
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                                                                                                   ---- Genome Center
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89356:
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111915:
112015:
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64946
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 TITLE
JOURNAL
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                                                                COMMENT
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Direct Submission

Submitted (16-07-2012) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, Qelo 15A, UK. E-mail enquiries:

Cambridgeshire, Qelo 15A, UK. E-mail enquiries:

humqueryesanger acuts Clone requests: clonerequest Gesanger.ac.uk

numqueryesanger.acuts Clone requests: clonerequest Gesanger.ac.uk

buring sequence assembly data is compared from overlapping clones.

Where differences are hound these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may het be found in the sequence submission colly a small overlap as deschibed above.

This sequence was finished as Kollows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve All sequencing problems, such one plasmid subclone or more than one Mil's subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature rable with their source databased; Ent. EMBL; Swi, SWISSPROT; Tr., TREMBL; Wpi, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5520 TCTGTTAGTAGGCCTTGTTCCTGCACCATGAGCATGATTATGAAGTTGTGTTTCCACAC 5461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL606804 185467 bp DNA linear PRI 23-OCT-2002 Human DNA sequence from clone RP11-978115 on chromosome 1, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5640 CCCCATCAGAGATCCTCCCTGAGCTCCAATGATGACGATAGAGAACATTGACACCCTC 5581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5580 ACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGGACT 5521
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5700 CAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGAAGTGCTACACTGTCATTAATCACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ProHisGlnArgSerSerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GlnGluAsnGluAsnGlySerGlySerGluGluValCysTyrThrValIleAsnHisI
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Mismatches:
Indels:
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ALEO6804.11 GI:24366459
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Strausberg, R
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                       TITLE
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1 (Bases I to 1521)

2 (Bases I to 1522)

3 (Bases I to 1522)

3 (Bases I to 1522)

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Homo sapiens germinal center expressed transcript 2, mRNA (cDNA clone MGC:40441 IMAQE:4385178), complete cds.
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group.

Purther information can be found at http://www.sanger.ac.uk/HGP/Chr1
RPII-978115 is from the library RPCI-11.4 constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAACe3.6
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens
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Best Local Similarity:
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SOURCE

REFERENCE AUTHORS

LOCUS

RESULT 9 BC030506

ACCESSION VERSION KEYWORDS

Query Match: DB:

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source

FEATURES

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USA

USA

USA

USA

UNH-MGC Project UNL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-romaih.nih.gov

Tissue Procurement: you Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing Center (NISC)

Marian Institutes of Health Intramural

Sequencing Center (NISC)

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ABEYTENVPCKARRPRESLGGTETEYSLLHMPSTDPRHARSPEDEYELLMFHRISSHP
LQQPRPLMAPSETQFSHL"
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Series: IRAK Plate: 64 Row: a Columni,15
This clone was sected for full length sequencing because it passed the following selection criterial matched mRNA gi: 22749536. Location/Qualifiers
MCKErnan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Valladon, D.K., Munzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Buyfiard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dikkson, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generataion and initial analysis of more than 15,000 full-length
human and mouse only sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submibgion
Submitted (07-4Mr-2002) National Institutes of Health, Mammalian
Submitted (07-4Mr-2002) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numan add mouse cDNA sequences
Proc. Marl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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/clone="MGC:40441 IMAGE:4385178"

/clone lib="Uymph, lymphoma"

/clone lib="NH MGC 85"

/lab host="DH10B"

/note="Vector: pCMV-SPORT6"
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Submitted (05-MAR-1992) Richard Treisman, Transcription Laboratory,
Imperial Cancer Research Fund, London, England
On Nov 29, 1993 this sequence version replaced gi:338036.
Original source text: Homo sapiens cDNA to mRNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI 17-DEC-1993
                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bureleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Momo.
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1 (Dasea It o. 1933)
Dalton, S. and Treisman, R.
Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element
(2) (5) (5) 7-612 (1992)
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Homo sapiens/SRF accessory protein lA (SAP-1) mRNA, complete cds.
M85165
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Bull,J.H., Ellison,G. and Paskins,L.D.
Diagnostic methods for the detection of prospete disorders
Patent: WO 0136674.A 20 25-MAY-2001;
AstraZeneca AB (SE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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1.3%; Score 49; DB 6; L.
Best Local Similarity 100 06; Pred. No. 5.6e-13;
Matches 49; Conservative 0; Mismatches 0;
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Homo Sapiens (human)
                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapieng"
|mol type="unassigned DNA"
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                                                                                                                                                                                                                                                                              Location/Qualifiers
1, .1933
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Treisman, R.
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Homo sapiens
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/tissue_type="from acute myelogenous leukemia"
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/lab host="DH108 (TI phage-resistant)"
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(ggccgttaeggcc); Doubhe-stranded cDNA was prepared from cell ine RNA. 5' and 3' adaptors were used in cloning as follows: S' and 3' adaptors were used in cloning as follows: S' and 3' adaptors were used in cloning as follows: S' and 3' adaptors were used in cloning as follows: S' and N - A, C, G, or T). Avarage insert size
l:65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length closes and was constructed by clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAAAGGAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCGATCAGAGATCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 TCCCTGAGCTCCAATGATGATGATGAGAACATTGACTCCCTCACAAGGAAAGTGAGA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 GGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TCCCTGAGCTCCAATGATGATGACTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGGAAATTATCTCCTGCGAAACTCAGTTGCCTGGGAGAAATCAAAAGAAGCCCAAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGITIAGAGAAAGGICAGAGACAGAATAIGCCCTTCTTAGGACTTCTGTTAGTAGGCCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 CAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGGACTTCTGTTAGTAGGCCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 6.1e-86;
Matches 405; Conservative 0; Mismatches 0; Indels 0;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetarriodactyla, Suina, Suidae, Sus.
1 (Dases 1 to 268)
Pahrenkrug, S.C., Safth, T.P.L., Freking, B.A., Cho, J., White, J., Quackenbush, and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and linear AW480906 33516 MARC 2PIG Sus scrofa CDNA 5', mRNA sequence AW480906 AW480906.1 GI:7050949 ester assembly Sus scrofa (pig) Sus scrofa LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS

TITLE

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/Jote="Homology region A with Elk-1 protein (Ets domain)
is bp 150-417, amino acids 1-89; Homology region B with
Elk-1 protein, required for cooperative terinary complex
formation with SRF is 565-617, amino acids 136-157;
Sequence diverges from SAP-1B at bp 1229, amino acid 360;
Homology region C with Elk-1 protein, core of regulated
transcription activation domain, is bp 1203-1355, amino
acids 352-402; 6371P motifs conserved between SAP-1A and
Elk-1 are located at amino acids 7354, 7360, 7366, S381,
S387, 7420, 8425, corresponding to bp 1209-1214, bp
1407-1412, bp-1422-1427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMSAPIA 1933 bp mRNA linear PRI 17-DEC-1993
HOMO Bapiens/SRF accessory protein 1A (SAP-1) mRNA, complete cds.
M85165
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominiges, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota) Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dase 1 to 1933)
Dalton, S. and Treisman, R. Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response cell 68 (3), 597-612 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                      Bull,J.H., Ellison,G. and Paskins,L.D.
Diagnostic methods for the detection of prostate disorders
Patent: WO 0136674-A 20 25-MAY-2001;
AstraZeneca AB (SE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.3%; Score 49; DB 6; Length 1933; Rest Local Similarity 196.0%; Pred. No. 5.6e-13; Matches 9; Conservative 0; Mismatches 0; Indels
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Berum response factor; SAP-1; Elk-1.
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ORGANISM

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GANTLEQUENTARGTANT
GANTLEDGESTLANGTH
GAN

0; Gaps Query Match Best Local Similarity 100.0%; Pred. No. 5.6e-13; Matches 49; Conservative 0; Mismatches 0; Indels

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DEGITTO-67...

OM nucleic

Run on:

Sequence:

Searched:

Database

Result

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Langua Papteura

Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (Bases I to 527)

I (Bases I to 527)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

Http://image.llnl.gov

Plate: LLCM993 row: a column: 01

High quality sequence stop: 518.
                                                                                                                                                                                                          AA311038 EST181808.
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BM459235 AGENCOURT
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BU746391 CH1948003 H
BU746391 CH1948003 H
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BU746392 CH24803 H
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BG276804 tu06606.y
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AY404586 Homo sapi
BQ214406 AGENCOURT
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     AY404586
BQ214406
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BM904106
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BM458336
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CD105480
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BG276846
CE207791
CB320849
CNS030Q4
CNS030Q4
AL5145055
BU32245
BU32245
BX367419
CE196251
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AW480906 33516 MAR
BF797507 602257174
BM455407 AGENCOURT
                                                                                                               April 22, 2004, 13:36:26; Search time 2525 Seconds (without alignments) 4789.775 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Homo sapiens (human)

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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1045)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Inc.

Contact: Robert Strausberg, Ph.D.

Contac
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60257174F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4340323 5',
BP797507
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   Genome 13 (8), 475-478 (2002)
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33516 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW480906.1 GI:7050949
                                      . .527
organism="Homo sapiens"
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clone="IMAGB:4109064"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Strautt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llni.gov
Plate: LiAM12135 row: d column: 24
High quality sequence start: 19
High quality sequence stor: 760.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 hacaalgeccaricagggaacricrgcrigaagagracrargagaaricccrigcaaagcrga 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 GAGACCCAGAGAGTCCTTGGGAGGAACTGAGACTGAGTATTCACTTCTACATATGCCTTC 506
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Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 1:867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Mammaliai Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 TGTTAGTAGGCCTTGTTCCTGCACCCATGAGTTATGAAGTTGTGTTTCCACAC 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 59.6; DB 10; Length 1045; Similarity 54.7%; Pred. No. 0.00075; Conservative 0; Mismatches 129; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                     organism="Homo sapiens"
High quality sequence stop: 687.
Location/Qualifiers
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Best Local S
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BM455407
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Note: this is a NIH_MGC Library."
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1 (bases 1 to 508)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, White, T.J., Shinsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 TGTTAGTAGCCCTTGTTCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTTCCACAC 405
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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14.5%; Score 58.6; DB 12; Length 1085;
Best Local Similarity 54.4%; Pred. No. 0.0013;
Matches 162; Conservative 0; Mismatches 130; Indels 6;
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/clone_lib="NIH_MGC_92"
                                                                                                                                                                                                    14.3%; Score 58; DB 29; Length 508; 54.4%; Pred. No. 0.0017; trive 0; Mismatches 130; Indels
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                                                                                                                                    114 AAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA 173
                                                                                                                                                                                                     174 CGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA 230
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/lab.host="DH10B (phage-resistant)"
/clone_lib="NIH WGG;
/clone_lib="NIH WGG;
/note="forgan: testis; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally; oligo-dT_primed.
Average insert size_2: Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Email: cgapbs-r@mail.nth.gov
Tissue Procurement: Arc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLMM10423 row: column: 01
High quality sequence stop: 726.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                        6; Gaps
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llarity 54.4%; Pred. No. 0.0018;
Conservative 0; Mismatches 130; Indels
Query Match

14.3%; Score 58; DB 13; Length 876;
Best Local Similarity 54.4%; Pred. No. 0.0018;
Matches 162; Conservative 0; Mismatches 130; Indele
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full-length, clones and constructed by Life Technologies.
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S', mRNA sequence.
                             174 CGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA 230
                                                           231 TCAGAGATCCTCCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAG 290
                                                                                                                                                                                           463 TACAAGGCCATCAGGGAACTCTGCTGAAGAGTATATGAGAATGTTCCCTGCAAAGCTGA 522
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                                                                                                                                                                                                                                                                                                      523 GAGACCCAGAGAGTCCTIGGGAGGAACTGAGTGTGTTCACTTCTACATATGCCTTC 582
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outputting A. (13); (Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg). Email: cgapbs-remail.nih.gov
Tissue Procurement: Low Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
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the Not I and Ecory sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 ENYY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1964.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi-seq-CSOBGO07CB08QPl&cluster=1964.r. Contact :

Feng Liang Email: fliangalifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSODG007CB08QPl.
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114 AAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA 173
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ALS60376 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODG007YD15 5-PRIME, mRNA sequence.
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1 (bases 1 to 987)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-langth, CDNA libraries and normalization
Unpublished (2001)
On Peb 15, 2001 this sequence version replaced gi:12906778.
                                                                                                                                                                                                                                                                                                                                                                                                                                          348 TGTTAGTAGGCCTTGTTCCTGCACCATGAGCATGATTATGAAGTTGTGTTTCCACAC 405
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14.3%; Score 58; DB 9; Length 987;
Best Local Similarity 54.4%; Pred. No. 0.0018;
Matches 162; Conservative 0; Mismatches 130; Indels
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi; Bukaryota; Mammalia; Buthoria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 1070)

S. NIH-MCC http://mgc.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

Long distribution: MGC clone distribution information can be from through the In M.A.G.E. Consortium/LiNL at:

Http://image.llnl.gov

Plate: LLAM12124 row: h column: 22

Http://image.llnl.gov

Plate: LLAM12124 row: h column: 22

High quality sequence stop: 648.
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                          AGENCOURT 6409034 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5496261
5', mRNA sequence.
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425 GAGACCCAGAGAGTCCTTGGGAGGAACTGAGACTAATTCACTTCTACATATGCCTTC 484
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14.3%; Score 58; DB 12; Length 1070;
Best Local Similarity 54.4%; Pred. No. 0.0018;
Matches 162; Conservative 0; Mismatches 130; Indels
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
E 1 (Bases I to 1039)
I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies of the Consortium (LINL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
High quality sequence stop: 665.
High quality sequence stop: 665.
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Joaquaism="Homo sapiens"

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                                                                                                                                                                                                                              461 GAGACCCAGAGAGGAGGAACGAACTGAGATTCACTTCTACATATGCCTTC 520
                231 TCAGAGATCCTCCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAG 290
                                                                                      401 hacaaggccarcagggaacrcrgcrgaagagracrargagaargrccrgccaaagcrga 460
                                                                                                                                                                 291 GAAAGIGAGACAGIIIIAGAGAAAGGICAGAGACAGAAIAIGCCCIIICI---IAGGACIIC 347
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RESULT 12 BG106563

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AGENICOURT 6405645 NIH_MGC_85 Homo saplens cDNA clone IMAGE:55001415', mRNA Bequence.
BM455198.1 GI:18504238
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/ Coganism=Thomo sapiens"

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/ Ab_xref="taxon:9606"

/ Clone="IMAGE:4342719"

/ Lissue type="lymphoma, cell line"

/ Lab_host="DH10B (phage-resistant)"

/ Clone lib=NHH MGC 85"

/ Actor lib=NHH MGC 85"

/ Actor liber insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
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BF795688 1124 bp mRNA linear EST 12-JAN-2001
602259560F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4342719 5',
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 1124)

S NIH-MGC http://mgc.nci.nlin.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plage to LLAM9958 row: h column: 16

High quality sequence stop: 715.
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14.3%; Score 58; DB 10; Length 1124;
Best Local Similarity 54.4%; Pred. No. 0.0018;
Matches 162; Conservative 0; Mismatches 130; Indels (
                                                                                                                    BF795688.1 GI:12100659
                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                nRNA sequence.
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//wol_type="m&NA"
//db xxef="texon:9606"
//db xxef="texon:9606"
//tissue_type="lymphoma, cell line"
//tissue_type="lymphoma, cell line"
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//clone_lib="NHH-MGC_85"
//note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
//worage insert size 1.867 %b. Library enriched for
full-length: clones and constructed by Life Technologies.
Note: this is a NH-MGC Library."
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                                                                                                                                1095 bp mRNA linear EST 30-JAN-2001
602290373F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385178 5',
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Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Prourement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 19
High quality sequence stop: 641.
                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1095)
NIH-MGC http://mgc.nci.nih.gov/.
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Best Local Similarity 54.4%; Pred. No. 0.0018;
Matches 162; Conservative 0; Mismatches 130; Indels
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Ovorak, C.M.T., Hyland, K.A., Zhang, Y., Fahrenkrug, S.C. and
                                                 Mulrowsy, v.r. Porcine jejunal Peyer's patch expressed sequences Unpublished (2003)
Conteact: Murtaugh, M.P.
Copartment of Veterinary PathoBiology
University of Minnesota
1971 Commonwealth Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
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                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 CGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 TCAGAGATCCTCCCTGAGCTCCAATGATGATGACTATGAGAACATTGACTCCCTCACAAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 TACAAĞGCCATCAGGĞAACTCTGCTGAAGAGTACTATGAĞAATGTTCCCTGCAAAGCTGA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AAAGAGGGAAGATTCCCAAAACGAAATGAAAGAATGTCATCTRCTCCCATCCAGGACAA 294
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                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: ogapbe-r@mail.nih.gov
Tissue Procurement: Low Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: Libralizia row: j column: 14
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="lymphoma, cell line"
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Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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Location/Qualifiers
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DRIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 15 CB286394

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/tissue type="Peyer's patch"
/clone Tib="UnrawPM3"
/clone Tib="UnrawPM3"
/clone Tib="UnrawPM3"
/clone Tib="UnrawPM3"
/pote="Organ: small intestine, jejunum; Vector:
pcWVSPORT6; Site 1: Not1; Site 2: Sall; Jejunal Peyer's
pcwCsport6; Site 1: Not1; Site 2: Sall; Jejunal Peyer's
pcross-bred pigs. RNA was extracted either immediately or
after 3 hours stimulation in an Ussing chamber with one of
the following treatments: 1) no treatment, 2) Salmonella
choleraeeuis vaccine strain SC-54, 3) phorbol myristate
acetate, concanavalin A, and 8-bromo-cyclic AMP, and 4)
lipopolysaccharide and cholera toxin. Each treatment was
performed in the presence and absence of cycloheximide.
Purified poly A + RNA from each of the treated tissues
(2-4) was combined together, reverse transcribed, and
cloned in to pcWVSPORT6 to make a library of approximately
530,000 recombinant clones with an average insert size of
1.0 kbp. Poly A+ RNA from freshly isolated and non-treated
tissue from an Ussing chamber (treatment 1) was cloned in
the same manner to produce an unstimulated colb. library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            approximately 900,000 clones with an average insert size of 1.5 kbp. Equal portions of the two libraries were pooled and then subtracted with porcine ST fibroblast RNA to create a subtracted porcine Peyer's patch library of approximately 6,000 clones with an average insert size of 1.0 kbp."
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TITICAAAAGAAAACTICAAGAICAAGAIAAGAAAAGCCAAGAAGITICAICCACTICIAAI 165 e F Query Match
14.2%; Score 57.4; DB 14; Length 526;
Best Local Similarity 51.8%; Pred. No. 0.0024;
Matches 155; Conservative 0; Mismatches 141; Indels 3 106 유 ઠે

ORIGIN

166 CAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATC 225 62 galgiala de de contra d 2 TTTAAAGCAAGACAAGATTCCCCAAAGCAAAATGAAGAAACATCATCTTCTCCTTCCAG 61

226 CCCCATCAGAGATCCTCCCTGAGCTCCAATGATG---GCTATGAGAACATTGACTCC 282 283 CTCACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGG 342 122 Accicriosolabasocicaaradocacicoriocióaosolociariolada Accirircionica 181

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182 AAGACCGAGAGGCCCAGAGAGTCATTGGGAGGAACGGAGACTGAGTACTCACTTATTCAT 241

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BC052102 Xenopus 1
BC004356 Homo sapi
BC004356 Homo sapi
BC004364 Homo sapi
BC0043714 Mus muscu
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BC043714 Mus muscu
BC040896 Homo sapi
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BC052305 Danio rer
BC052972 Danio rer
AX026959 Homo sapi
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AX1381 Pequence
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AR300635 Sequence
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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87.3 4032
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Copyright (c) 1993 - 2004 Compugen Ltd.
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139 48 1.3 1572 5 BC053234 BC0653234 Danio rer. 140 48 1.3 1584 3 AK112206 AK112206 Ciona int. 141 48 1.3 1594 9 AF035321 AF035321 Homo sapi. 142 48 1.3 1680 9 BC053634 BC053634 Homo sapi. 144 48 1.3 1711 9 BC0471159 BC0471159 Homo sapi. 145 48 1.3 1729 5 BC047834 AX35878 Sequence. 147 48 1.3 1837 6 AX358786 AX362279 Sequence. 148 48 1.3 1837 9 AX358545 Homo sapi. 149 48 1.3 1850 9 BC038983 BC038983 Homo sapi. 150 48 1.3 1923 9 BC028199 Homo sapi.	RESULT 1 AX50512 10CUS AX505122 3762 bp DNA linear PAT 27-SEP-2002 DEFINITION Sequence 1 from Patent W00246389. VERSION AX50512. VERSION AX50512.1 GI:23386429 KEYWORDS	SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; heas Bukaryota; homosapiens Bukaryota; homosapiens Bukaryota; butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Nocka,K., Pirozzi,G. and Einstein,R. TITLE activation JOURNAL Patent: WO 0246389-A 1 13-JUN-2002; UCB, A.A. (BE) Location/Qualifiers Source /organism="Homo sapiens" /mol type="Homo sapiens" /mol type="Unassigned DNA"	CDS 25.432 25.432 / db_xref="taxon:9606" 25.432 / note="unnamed protein product" / codon start=1 / codon start=1 / protein_id="CAD48808.1" / db_xref="de"(AD48808.1" / db_xref="TEWTREMED:CAD48808" / db_xref="TEWTREMED:CAD48808" / db_xref="TEMTREMED:CAD48808" / db_xref="TEMTREME	1 GAGAAACCGAGTCATGTGAAAATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTG 1 GAGAAACCGAGTCATGTGAAAAATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTG 2 GAGAGAATCAAAAAAAAAAAAAAATGGAAATTATCTCCTGCGAAAACTCAGTTGCCTG 6 GGAGAGATCAAAAGAAAGAAAGAAAACCAAATGAGAAAACCGAAAAAAAA
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TTTCCACACTAAAATCCTCAAACATTATATCACCTTCCAGCAATGAAGACAATGAAGAAAAAAAA	<i>&</i> 93	1501 CTCAATAAACTGTGTAAGACCAGTGACCAGACCCTTTGCTAACCTCACATTTACTTCAAT 1560
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AAGTTTAGAAATATTATTATTATATATATCTTAGGCAACTTCTGATATGGCATCTCTG	ර් අ	1621 TAATAGTTTTTGACATTGGCTTTTCTGAGAAGAGAAATTGAAAGTGTCACAAAATAAAA 1680
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TGAAAATATTTTTAATCCCCCTGACTAACTGAATGGACCCTCTTTTGAGCCCAAAGGACCCCCAAAGGACCCCGAAAGGAAAAAAA	S do	1861 TICTGGTTTTAAATTCAAGCAAACTGGAAAATAATCCATCTAATTATGCTTTCTTCCC 1920
TIGITATACCCCTTCCCTTTTGGAGTTATGCACAGGAGCCAGGAGCCAGGAGCCAGGACCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGG	Q. O.	1921 AAGAAGTITITTAATGATATGCCAGCTTCCTAATTTGGAGACAAAAGCCTTAATTGACAA 1980
TIGITATACCCCTTCCCTTTTGGAGTTTATGCACAAGTGACCAGGATGAGTCAGGATGAAGT 9 GATGABATAGACTGATTGTGGGCAATAAGAGTCCCAATTCCAACTGACTCTGGTGTAGAT 9	S G	1981 IGCAITCAITATAITTITTITATATACATACAGTATACGAGTIGAGTATCCCTTAGATG 2040
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Pred. No. 0;
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Best Local Similarity 99.8%;
Matches 3526; Conservative
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              Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0%
Assembly program: Phrap; version 0.990319
Consenus quality: 136274 bases at least Q00
Consenus quality: 138356 bases at least Q10
Consenus quality: 139182 bases at least Q20
Insert size: 142000; agarose-fp
Insert size: 140368; sum-of-contigs
Quality coverage: 4.64 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                 1377: contig of 31377 bp in length
1378 31477: gap of unknown length
1312 64845: contig of 31534 bp in length
1312 64845: contig of 1734 bp in length
1314 64845: contig of 1734 bp in length
1346 6766: contig of 1734 bp in length
1346 6766: contig of 2661 bp in length
1347: contig of 2661 bp in length
1347: contig of 9968 bp in length
1347: contig of 9968 bp in length
1357: contig of 11442 bp in length
1357: gap of unknown length
1356: gap of unknown length
1356: gap of unknown length
1351: contig of 11415 bp in length
1357: contig of 11415 bp in length
1358: contig of 11415 bp in length
1351: contig of 18458 bp in length
1351: contig of 18455 bp in length
141268: contig of 18455 bp in length
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141268: contig of 18485 bp in length
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70056-assembly_name:Contigs"
89357. 100400 / note="assembly_name:Contig6"
100501. 111915 / note="assembly_name:Contig7"
112016. 125713
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67707. .77674
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    Summary Statistics
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1029 4861 1089 1148 4742 4682 1268 5041 5641 5581 5341 5221 5101 4921 4860 CCTTTATTTTACGTAAAGCATTCTTTTCTACTGACTTCTTAAGTCTTTAGACAAAGCTTA 4801 5461 5401 5281 729 789 696 549 609 849 606 309 369 429 489 699 ACTCTTTCAACCAATTGCCAATC-AGACAAACTTTGAATCTACCTATGACCTGTAAGCTC 1920 TCTGAGGGATTCCATCTATGAGACTTTGTCTACATAACAGAGACCTTGGTTTCCACAACC 730 ATTICIDATICCCCTGACTAACTGAATGGACCCTCTTCTAGGCCAAAGAGACCTCAGATG 5160 ATTTCTAATCCCCCTGACTAACTGAATGGACCCTCTTCTAGGCCAAAGAGACCTCAGATG 910 GACTGATTGTGGCAATAAGAGTCCCAATTCCAACCTGACTCTGGTGTAGATCACACTG TCTGAGGGATTCCATCTATGAGACTTTGTCTACATAACAGAGCCTTGGTTTCCACAACC 4800 ACTCTTCAACCAATTGCCAATCNAGAC-AACTTTGAATCTACCTATGACCTGTAAGCTC TTATGTCTTTGCTTGTAACTCCTGTCTCCCTAAAATGTATAAAAGTAAAAGGGTGACCTG 5520 TCIGITAGTAGGCCTTGTTCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCCACAC 5460 TAAAATCCTCAAGCTGCTTTATCACCTTCCAGCAATGAAGACAATGCAGAATAGCAGACT 550 AATATTATCTTATTATATCCTTAGGCAACTCTGATATGTGGCATCTCTGTGGCTTAGG 5280 TGBAATCATAGAAATTGACACAATGACCTAAAATATTCTATGTGTTTTTGCTTGTAAAGT TCTCCTGCTTCAAGATCTTGCCTCTTTAAGCTGAACCGATGTGCACTTTCCATTTAATGA 5700 CAGGAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACAT s640 ccccarcagadarccrcccrcadecrccaargargargacaragadaacarrgacrccrc 310 ACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGGACT 370 TCTGTTAGTAGGCCTTGTTCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCCACAC 430 TAAAATCCTCAAGCTGCTTTATCACCTTCCAGCAATGAAGACAATGCAGAATAGCAGACT CTGGCTAAAGTTTAGA 610 TGAAATCATAGAAATTGACACAATGACCTAAAATATTCTATGTGTTTTTGCTTGTAAAGT TTGAGGACATGGAGGTGATAAAAAAACTTTCTTAGGACAATAATGTAAAATGAAAATAA 790 AACCIGAAAGACIGAAIICIGGCCAIGAIAGGAAGGGAGGIGAGACACACCCIIGIIAIAC CCCTTCCCTTTGGAGTTTATGCACAAGTGACCAGGATGAGTCATAAGACTGAAATA CCTTTATTTTAGCTAAAGCATTCTTTTCTACTGACTTCTTAAGTCTTTAGACAAAGCTTA 190 CAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATC 250 CCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGATGAGGCTATGAGAACATTGACTCCCTC

2419 CTTTGGGAAACCAAGACCAAGACTCTTGAGCCCAGAATTTGAGCCCAAGATTGACCAAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGACCCAGAATTTGAGCCAGAATTTAGAATTTAGAATTTGATTAGAATTTGATTTAGAATTTAGAATTTGATTAGAATTAGAATTAGAATTTAGAATTTAGAATTTAGAATTTAGAATTTAGAATTTAGAATTTAGAATTTAGAATTTAGAATTAGAATTTAGAATTTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAATTAGA
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/db_xref="Locus1D:148823"
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KKSQEVSGTSNQENSTRGSGSEEVCYTVINH.PHQRSSLSSNDDGYENIDSLTRKVRQF
RRRSETEYALLRTSVGRPCSCTHEHDYEVVPPH"
                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 32 Row: b Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21687148. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTAGGACTTCTGTTAGTAGGCCTTGTTCCTGCACCCATGAGCATGATTATGAAGTTGTG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GACTCCCTCACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTT
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Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2606; Conservative 0; Mismatches
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Riausberg, R.L., Feingold, E.A., Magner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Garcia, A.M., Madan, A., Rodrigues, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNa sequences

NELSHERS, S. M. Schein, J.E., Jones, S.J. and Marza, M.A.
Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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Homo sapiens LOC148823, mRNA (CDNA clone MGC:24564 IMAGE:4109064),
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
1 (bases 1 to 2648)
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Submitted (19-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
       CCCTGAGTTTCACCAGTCCTGGCAACCAATGATCTGCTTCGTATAATTATAACTGTTCTA
                                 CCTGAGTTTCACCAGTCCTGGCAACCAATGATCTGCTTCGTATAATTATAACTGTTCTA
                                                                                                     CATTATAATATTTTTGAGATTCATCTATGTTTAATGTTCTATCAGTAGTTGTACATCTTA
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Tissue Procurement: ATC:
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories Inc.
CDNA Library Preparation: CLONTECH Laboratories
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
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Contact: MGC help desk
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Db 1644 TAATAGTTTTTGACATTGGCTTTTCTGAAAGAAATTGAAAGTGTCACAAAATAAAA 1703 Oy 1681 AAGATGAAATGAAGCATATATAATTTTTTTTTTTTTTTT	CY 1741 GAAGGATTCTGTTCAAATTAGTAAAAATTGAAAATAAACTTGTGCTTATATTTTGTTT 1800 DD 1764 GAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATTGAAAATTTGTGTTT 1823	186	1861 ITCTGGTTTTAAAATTCAACCAAACTGGAAAATAATCCATCTAATTATGCTTTCTCC 19 1884 ITCTGGTTTTAAAATTCAAGCAAACTGGAAAATAATCCATCTAATTATGCTTTCTTT	1921 AAGAAGTTTTTTAATGATATGCCAGCTTCCTAATTTGGAGACAAAAGCCTTAATTGACAA 1	TGCATTCATTATATATTTTTTGTATAGATTACAGTATGCGGTTGAGTATCCCTTAGATG 	2041	2101 CCATACATATATATATATATATATATATATATATATATA	2161 TGTTTGATACACCTTATCTGAATAGCCTGAAGGTAATTTTATACATATTATAAATAA	2221 TTTTATGCCTGAAACAGATTTGCGCACATTGGACCATCAGAAGCAGAAGTGTCACTAT 23	2281 TTCAAGTGGTGAAAAGTTTCAGATGTTAAGCTGGTGATGCAGTTCATGCCAG 2304 TTCAAGTGGTCAAAAGTTTCAGATGTTAAGCTGGTGATGCAGTGTTAAGCTGGTGATGCCAG	2364 TCCGAGTACTTTGGGAAGCCAAGAGCGGGGTCTTGAGCCCAGGGTTTGAGGCCAGGTTTGAGGCCAG 242	2424 ACTGCACAACACAGTGAGACCTCGTTTCTACAAATAATTAAAAATTAGCCAGGTGTGGT	2484 GGTGCACACCTGTAGTCCCAGGTACTCAGGAGGCTGAGGTAGTAGTAGTTGTTTGAGACTG	11	2604 TGAGACCCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAA	9	Homo sapiens cuna Flutisus IIB, cione Novakzuouri AK123798 AK123798.1 GI:34529425
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4 AAGITIAGAAATAITAICITATATATATCCITAGGCAACTCIGAIAIGIGGGCAICTCIG 1 TGGCTTAGGTGAAATCATAGAAATTGACACAATGACCTAAAATATTCTATGTGTTTTTTGC	24 TGGCTTAGGTGAAATCATATAATTGACACAATGACCTAAAATATT 61 TTGTAAAGTTTGAGGACATGGAGGTGATAAAAAAAAACTTTCTTAGG		CTTCAGATGAACCTGAAAGACTGAATTCTGGCCATGATAGGAAGGGAGGAGTGAGACACACAC	841 TIGITATACCCCTTCCCTTTTGGAGTTTATGCACAAGTGACCAGGATGAGTCATAAGACT 900 		CACACACTGTCTGAGGATTCCATCTATGAGACTTTGTCTACATAACAGAGACCTTGGTT 1	1021 TCCACAACCCCTTTATTTAGCTAAAGCATTCTTTTCTACTGACTTCTTAAGTCTTTTAGA 1080 1044 TCCACAACCCCTTTATTTTAGCTAAAGCATTCTTTTCTACTGACTTCTTAAGTCTTTAGA 1103	1081 CAAAGCTTAACTCTTTCAACCAATTGCCAATCAGACCATTGAATCTACTATGACCT 1140 	1141 GTAAGCTCTCTCCTGCTTCAAGATCTTGCCTCTTTAAGCTGAACGGATGTGCACTTTCCA 1200	01 TTTAATGATTATGTCTTTGCTTGTAACTCC 	1261 GIGACCIGACCACCTCAGGCACACTITCTCAGGACCTCCTGAGAGTGTATCCCAGGCCAT 1320	1321 GGTAAGTCAIGTIGGCTCAGAATCAACCTCTTTAAATATTTTACAGAATTTGGGTTTTGG 1380 	1381 TTACCAATAAGTCTCCACAAATATATGTCCAAGAATCTTCAATTCCAAGCCTGCTCACCA 1440 	1441 AATTICAAAIGCCAACAICTCCCCAICCAAITACCIAITICAICITIGAGGIGIAAICIA 1500 	1501 CTCAATAAACTGTGTAAGACCAGTGACCAGACCCTTTGCTAACCTGACATTTACTTCAAT 1560 	1561 TITICTTITICTAIGTACTGGATATTTTTGCATATAAACTTGCAGTAATAGTTCAAAAT 1620 1584 TITICTTTTCTATGTACTGGATATTTTTGCATATAAACTTGCAGTAATAGTTCAAAAT 1643	21 TAAT
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λà	106	GATGADAITAGACTGATTGTGGGAATAAGAGTCCCAATTCCAACCTGACTCTGGTGTAGAT 960
q	935	GAIGAAATAGACTGATTGTGGGAATAAGAGTCCCAATTCCAACTGTGACTCTGGTGTAGAT 994
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O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pienni,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Tresfaye,S., Theodore,J., Tirell,A., Travers,M., Trajillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Voung,G., Zainoun,Y., Zimmer,A. and Zody,M.

Direct Submission

Submitted (24-ANG-2002) Whitchead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 5, 2000 this sequence version replaced gi:6970536.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fcp.genome.washington.edu/RW/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This record contains 134 individual
* sequencing reads that have not been assembled into
* contiggs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L5247
Center clone name: 482_N_10
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Direct Submission

Direct Submission

Submitted (14-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Sloases 1 to 121353)

RS Birren,B. Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwih,J., Barna,N., Basten,V., Bacda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Cheepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Diaz,T.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Kartes, M., Grand-Pierre,M., Grant,G., Hagos,B., Handers,T., Horton,L., Kartes,A., Kain,J., LaRocque,K., Lamazares,R., Landers,T., Horton,L., Kartes,A., Kain,J., LaRocque,K., Lamazares,R., Landers,T., Lehozzky,J., Levine,R., Lieu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McRena,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
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Signature of the control of the control of control of
                                                                    1475 AAITICAAAIGCCAACAICICCCAICCAAITACCIAITICAICTITGAGGIGTAAICTA 1534
                                                                                                                                                                                                  CTCAATAAACTGTGTAAGACCAGTGACCAGACCCTTTGCTAACCTGACATTTACTTCAAT 1560
                                                                                                                                                                                                                                                                                1535 CTCAATAAACTGTGAAGACCAGTGACCAGACCTTTGCTAACCTGACATTTACTTCAAT 1594
                                                                                                                                                                                                                                                                                                                                                                                 1561 TTTICTTTTTCTATGTACTGGATATTTTTGCATATAAACTTGCAGTAATAGTTCAAAAAT 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                           1595 TTTTCTTTTTCTATGTACTGGATATTTTTGCATATAAACTTGCAGTAAATGTTCAAAAT 1654
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                   1441 AATITCAAATGCCAACATCTCCCCATCCAATTACCTATTTCATCTTTGAGGTGTAATCTA 1500
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-482N10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1621 TAATAGTTTTTGACATTGGCTTTTCTGAGAAGAGAAATTGAAAGTGTCACAAAAT 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1655 TAATAGTTTTTGACATTGGCTTTTCTGAGAAGAGAAATTGAAAGTGTCACAAAAT 1709
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HOMO Sapiens chromosome 1 clone RP11-482N10 map 1, LOW-PASS
SECUENCE SAMPLING.
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Homo sapiens (human)
Homo sapiens
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                                          Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choppel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Dodlins, S., Collymore, A., Cooke, P., Fenestor, J., Ferraira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hasford, A., Horton, L., Karatas, A., Klein, J., Langocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Mcarkhy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Mennel, L., Minova, T., Miranda, C., Mlangan, V., Morrow, J., Naylor, N., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Yeung, G., Zainoun, J., Zimmer, A. and
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All repeats were identified using RepeatMasker:
All repeats were identified using RepeatMasker:
Attraction of the control of the
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
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COMMENT

AB060908 1924 bp mRNA linear PRI 10-JAN-2002 Macaca fascicularis brain cDNA clone:QtrA-14007, full insert

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

ABÓ60908 ABO60908.1 GI:13874585 Olgo capping; fis (full insert sequence) Macaca fascicularis (crab-eating macaque) Macaca fascicularis

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

sequence.

LOCUS DEFINITION

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Deada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Hirai, M.,
Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
Prediction of unidentified human genes on the basis of sequence similarity to novel CDNAs from cynomolgus monkey brain Online Publication

Genome Biology 2001 3(1): research0006.1-0006.5;
http://genomebiology.com/2001/3/1/research/0006/
E. 2 (bases 1 to 1924)
Black Submission

Direct Submission
Submitted (27.AR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1181)
Lab host: TOP10

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

JOURNAL

TITLE

REMARK

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Vector:

R. Site: Drall (CACTGTGTG)

[ATGTGGCCTTTTTTTTTTTTTTT], double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil digested PCR product was cloned into distinct Drall sites of pME182-F13. Khof sites just outside were constructed by oligo-capping method (Sugano et al., Institute of Medical Science, University of Chief. Control of Medical Science, University of Chief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248. .. 559

Codon_estart=1
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(5' end primer [CTTCTGCTCTAAAAGCTGCG];
3' end primer [CGACCTGCAGCTCGAGCACA]).
Location/Qualifiers
1. 1924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17485 AAATATGTCAGTCCTGTAGATATTAGCCAATTTTAGGAAAATGACAAAATTTTTTACTTT 47426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2836 AAATATGTCAGTCCTGTAGATATTAGCCAATTTTAGGAAAATGACAAAATTTTTTACTTT
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2896

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Length 1924;

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Score 106; DB

2.8%;

Query Match

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AL Submission

AL Submission

Direct Submission

Submitted (31-2AN-2003) Whitehead Institute/MIT Center for Genome Research, 230 Charles Street, Cambridge, MA 02141, USA

(bases 1 to 144333)

Estren, Anachoni, H.M., Barna, N., Bastien, V., Bloom, Y., Anderson, S., Arachoni, H.M., Barna, N., Bastien, V., Bloom, T., Boduslavkiy, L., Boukhgalter, B., Corum, B., Derstellano, K., Cook, A., Cook, P., Corum, B., Derstellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Graham, J., Grand-Pierre, N., Hagopian, J., Gardyna, S., Graham, J., Grand-Pierre, N., Hagopian, J., Gardyna, S., Graham, J., Grand-Pierre, N., Hagopian, J., Gardyna, S., Lindblad Toh, K., Liu, G., Lui, R., Indepor, J., Manclean, C., Macdonald, P., Major, J., Manchews, C., McCarthy, M., Maddrim, J., Mancus, L., Manning, J., Matthews, C., McCarthy, M., Maddrim, J., Mencus, L., Mihova, T., Munga, V., Murphy, T., Naylor, J., Schuper, S., Schupe, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Spencer, B., Schupe, C., Spencer, B., Schupe, C., Travers, M., Vassiliev, H., Vonkataraman, V.S., Travers, M., Vassiliev, H., Vonkataraman, V.S., Travers, M., Vassiliev, H., Vonkataraman, V.S., Travers, M., and Zody, M. Direct Submission
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Direct Summission

Submitted (13-WAR-2003) Whitehead Institute/MIT Center for Genome Submitted (13-WAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 13, 2003 this sequence version replaced gi:27753682.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT center for Genome Research

Center: Project was equence submissions@genome.wi.mit.edu

Center project name: 123019

Center project name: 2323_K_18
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543. 540
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/rpt family="Alux"
complement (1442. 1741)
/rpt family="Alusp"
complement (1823. 1962)
/rpt_family="FIAM_C"
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ement (Annual)
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                                                                                                                 1010 AGACCTTGGTTTCCACAACCCCTTTATTTTAGCTAAAGCATTCTTTTCTACTGACTTCTT 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                AC105036 144333 bp DNA linear PRI 13-MAR-2003 Homo sapiens chromosome 15, clone CTD-2323K18, complete sequence.
                                                                                                                                                                         1134 AGACCTTGGTTTCCACAACCCCTTTATTTTAGCTAAAGCATTCTTTTCTACTGACTTCTT 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (bases 1 to 14433)
Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone CTD-2323K18
                                                          Gapa
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                                                                                                                                                                                                                                                                              1194 AAGTCTTTAGACAAAGCTTAACTCTTTCAACCAATTGCCAATGAGA 1239
                                                                                                                                                                                                                                          1070 AAGICITIAGACAAAGCITAACICITICAACCAATIGCCAATCAGA 1115
                                                       0; Indels
                             100.0%; Pred. No. 1.7e-41; ative 0; Mismatches 0;
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                             Best Local Similarity 100.(
Matches 106; Conservative
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SOURCE
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AUTHORS
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AC105036
LOCUS
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

12 (Dases 1 to 217)

13 (Dases 1 to 217)

14 (Dases 1 to 217)

15 (Pobo,G., Han,M. and Wiemann,S.

15 (Pobo,G., Han,M. and Wiemann,S.

16 (Dase from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email 8 wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKF2p686G1888) is available at the RZEDD in Berlin. Please contact the RZEDD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlotterburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at thtp://mips.gsf.de/proj/CDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis similar to anterior gradient 2 homolog (Kenepus laevis), mRNA (cDNA clone MGC:53762 IMAGE:5537106), complete cds. BC052102.1 GI:30704994 MGC.
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Homo sapiens mRNA; cDNA DKFZp686G1888 (from clone DKFZp686G1888).
BX537812
BX537812.1 GI:31873786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
1 (bases 1 to 784)
2441 AAAAATTAGCCAGGTGTGGTGGTGCACACCTGTAGTCCCAGGTACTCAGGAGGCTGAGGT
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Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 52; Conservative 0; Mismatches 0; Indels
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1.6%; Score 62; DB 9; Length 144
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 62; Conservative 0; Mismatches 0; Indels
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complement(17006. .17310)
/rpt_family="LiMc4"
/rpt_family="Alusg"
complement'1...
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17pt family="Alusc"

Complement (12433. .12761)

/rpt family="Alusc"

/rpt family="Alusc"

13082. .13193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement(15492...15786)
/rpt family="Alusx"
/rpt family="15936
/rpt family="LiME4a"
16276...16434
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complement(9467...9627)
/rpt family="AluJ"
/rpt family="AluJ"
/0327...10459
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rpt family="AluSg/x"
omplement(17337. 17576)
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ement (17575)
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ement(1774°
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8199. .18501
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/rpt family="MIR"
16485 1677
1648 family="AluSx"
16772. 1679
/rpt family="(TTAA)n"
/rpt family="(TG802. 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13705. 14081

/ppt family="12"

/rpt family="Alusx"

14974. 15032

14974. 15032

15037. 15350

/rpt family="LIME4a"

15551. 155491

/rpt family="LIME4a"

/rpt family="LIME4a"
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/rpt family="AluSg"
19238. .19407
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19496. .19626
/rpt_family="AluY"
19928. .19955
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3194. 13409
rpt_family="L2"
3410. 13704
'rpt_family="Alu8x"
'rpt_family="Alu8x"
'3705. 14081
                                              7361 7432
7361 7432
7rpt family="(CA)n"
complement (9387...9
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family="MER5A"
 /rpt_family="MIR"
5933. .6118
/rpt_family="MIR"
7361. .7432
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M., B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Araminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallek, J.A., Gunarathe, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-MAY-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P. Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative
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Context: XGC help desk
Email: cgapbs-remail.nih.gov
Iissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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roc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db_xref="taxon:8355"
/clone="MGC:33762 IMAGE:5537106"
/tissue_type="Embryo, stage 31/32, Xenopus"
/clone_lb="NICHD_XGC_Emb4"
/lab_host="DH10B"
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1. .784
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/organism="Xenopus laevis"
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lein, S. and Strausberg, R.
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Homo sapiens chromosome 4 open reading frame 9, mRNA (cDNA clone
IMAGE3336655), partial cds.
                                                                                                                                                                                                                                                                                             /translation="MESVLKSIFVLLVATSFTLAKEIPAKVSKPQTLSRGWGDNLEWV
QTYBEGLYKAXAENKPLMLINHRNDCPHSLALKKAFAEHQGIQKLAEEFILLNVVYDP
TDKNLQLDGQYVPKIIFVDPSLVVRADLPGKYSNHQYTYEPADIDHLFENMKKALVLL
KTEL"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (02-UDL-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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On Aug 19, 2003 this sequence version replaced gi:14602504.
Contact: MGC help dis sequence version replaced gi:14602504.
Email: agapba remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Hubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                         /product="MGC53762 proteir
/protein_id="AAH52102.1"
/db_xref="G1:30704995"
/db_xref="LocusID:379407"
'db_xref="LocusID:379407"
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                                           19.<sup>7</sup>.513
/codon_start=1
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Clone distribution: MGC clone distribution information can be found
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Strausberg, R.
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Homo sapiens mRNA; cDNA DKFZp686M0187 (from clone DKFZp686M0187).
BX647746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAAPESYEELRSLLGRSMEEQLLVVERIOKCHIPSLAEGNKAXLEKLFGFLLEYVGD
TATDDPPDIVTUDKUVHLYHCQMPESSASDRI KTVLADAMERMEEME TRKGRAALP
GLDVLIYLKTTGLLPPTSDFMEPVVPPALVCLSQLINKCPILSLQDVKGLFVCCLFL
EYVALGORFIPBELINFLLGLLYIATPNKASQGSTLVHPFRALGKNSELLVVSAREDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 14 Row: j Column: 14.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYDWAYRELGPEMKAQPSNRWITEAELAKEEOEHLRKILEAERLRRMLGKDEDENVKKP
KEMSADDLINDGFVLDKDDRRLLSYKDGKAAVEEDVQEEQSKEASDPESNEEEGDSSGG
EDTEESDSPDSHSDLESNVESEEENEXPAKEQRQTPGKGLISGKERAGKATRDELPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="LocusID:8602"
'translation="QAQREDALELTEKLDQDWKEIQTLLSHKTPKSENRDKKEKPKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 570)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1379
//gene="Cdorf9"
/note="Nop14; Region: Nop14-like family. Emg1 and Nop14
are novel proteins whose interaction is required for the
maturation of the 185 rRNA and for 40S ribosome
DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                            | ... 1815.
| /organism="Momo sapiens"
| /mol type="mrnNa" |
| /db xref="taxon:9606"
| /clone="IMAGB:3936555"
| /tissue type="Lung, small cell carcinoma"
| /clone lib="NIH MGC 7"
| /lab_host="DH10B-R"
| /note="Vector: poIB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1815;
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100.0%; Pred. No. 1.8e-14;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="C4orf9 protein"
protein_id="AAH09760.2"
db_xref="G1:33874764"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db xref="CDD:pfam04147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonym: RES4-25"
/db_xref="LocusID:8602"
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                                                                                                                                                                                                                                                                                                                                                                                                                                gene="C4orf9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="C4orf9"
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Homo sapiens
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hes 52; Conserv
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SOURCE
ORGANISM
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VERSION
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LOCUS
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/db_xref="taxon:9606"
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/dev_stage="adult"
                                                                                                                                                                                                                                                               German Genome Project.

This close (DKF2056eM0187) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Kzzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Nacasja van den Bosch, Jilf Stott,
George Yang, Scott Zuyderduyn, Marco Marra.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (09-7AN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Direct Submission
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANN
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ), Email s.wiemann@dkfz.heidelberg.de;
sequenced by DKEZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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NHH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Thsue Procurement: Life Technologies, Inc.
Thsue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies,
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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100.0%; Pred. No. 2e-13;
ive 0; Mismatches 0; Indels
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (basea 1 co. 1589)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Riausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Wang, J., Haish, F.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Gasavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,

Carninoi, F., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Madan, P.J., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whithing, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whithing, M., Madan, A., Schwutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Stalaka, U., Sanilus, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

Human and mouse CDNA sequences

But Stages S. Marsywinski, M.I., Stages S. Sanchez, S. Marson, A.C.,

Butterfield, Y.S., Krzywinski, M.I., Stalakes, U., Sanilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Butterfield, Y.S. Krzywinski, M.I., Stalakes, U., Sanilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Butterfield, S. Starywinski, M.I., Stalakes, U., Sanilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Butterfield, S. Starywinski, M.I., Stalakes, U., Sanilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Butterfield, S. Starywinski, M.I., Stalakes, S. Sanilus, S. Starywinski, M.I., Stalakes, S. Starywinski, M.I., Stalakes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1589 bp mRNA linear PRI 03-OCT-2003
Homo sapiens hypothetical protein FLJ23306, mRNA (cDNA clone
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FLWKHWDALESYVERPFSSPR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadangesystemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuraa Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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On Aug 19, 2003 this sequence version replaced gi:14286207.
Contact: MGC help desk
Email: cgapbs-remmail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                  Length 1581;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                         1.3%; Score 50; DB 9; Le
100.0%; Pred. No. 1.8e-13;
tive 0; Mismatches 0;
      'db_xref="GI:28174969"
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Strausberg, R.
Direct Submission
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Best Local Simi
Matches 50;
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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BC008899
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Nobsite: http://www.hgsc.bcm.tmc.edu/cdna/
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-UUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAK Plate: 52 Row: d Column: 8.
through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
Series: IRAK Plate: 87 Row: h Column: 16.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procuremant: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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/protein_id="AAH34284.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOU94284 11near PF
HOMO sapiens, clone IMAGE:4779154, mRNA, partial cds.
BC034284
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.3%; Score 50; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 50; Conservative 0; Mismatches 0;
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/lab_host="DH10B"
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Direct Submission
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ACCESSION
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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BC034284
LOCUS
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source
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AUTHORS
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JOURNAL
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Mus musculus

I (bases 1 to 1616)

Strausberg, E.L., Feingld, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,
Hopkins, R.F., Jordan, H., Moore, A.A., Rubin, G.M., Haieh, F.,
Diatchenko, L., Marulana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcla, A.M., Gay, L.J., Hulyk, S.W.,
Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC043714 Hinear ROD 17-JUN-2003
Mus musculus RIKEN cDNA 2210023F24 gene, mRNA (cDNA clone
IMAGE:5371995), partial cds.
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NSWPELSLWLVAHAPFLVVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 24 Row: j Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13375679.
Location/Qualifiers
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100.0%; Pred. No. 1.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                       db_xref="LocusID:79579"
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                                                                                                                                                                                                                                                                                                     note="Vector: pOTB7"
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                                                                                                                                                                                                                                                                                                                                                 gene="FLJ23306"
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BC043714.1 GI:27881647
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Dest Local Similarity 100.0
Matches 50, Conservative
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KEYWORDS
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BC043714
LOCUS
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MEDLINE
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FLOLFGTKGVKRVLCPINYPESPTRFTHCEGVLGEGALDRGTYYWEVEIIEGWVSVGV
MAEGFSPQEPYDRGRLGRNAHSCCLOMNGRGFSVWFCGLEAPLPHAFSPTVGVCLEYA
DHALAFYAVRDGKLSLLRRLKASRPRRSGALASPTDPFQSRLDSHFSGLFNHRLKPAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 86 Row: o Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27369801.
Location/Qualifiers
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Direct Submission
Submitted (10-7AN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                               WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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1.3%; score ov, 2.1.3
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 50; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6"
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/organism="Mus musculus"
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RESULT 20 BCO56324 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

```
WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford Human Genome
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                              /codon_start=1
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REGISSITRSGVRSSPVREADMLASERSRDSSPKITDGNTDMKEREVQVWFQNRA
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LQLDSAVAHAHHILHSHLAAHAPYNMFPAPPFGLPLATLAAESASAASVVAAAAAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1654)
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 88 Row: 1 Column: 19.
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Submitted (06-DEC-2002) National Institutes of Health, Mammalian
Submitted (16-DEC-2002) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502. .672
/note="homeobox; Region: Homeobox domain"
/db_xref="CDD:pfam00046"
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/clone="IMAGE:5742758"
/tissue_type="Brain, adult medulla"
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clone="MGC:65884 IMAGE:6800994"
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Homo sapiens, clone IMAGE:5742758, mRNA.
BC040896
                                                                                                                     note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNKNSSIADLRLKAKKHAAALGL"
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                                                                                                                                                          .107
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AUTHORS
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JOURNAL
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BC040896
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(Ypriniformes; Cyprinidae; Danio.

(Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Rauser,R.D., Collins,P.S., Wagner,L., Shemmen,C.M., Schuler,G.D., Altschul,S.P., Zeeberg,B., Buttow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K.P., Fanade,C.F., Banaldo,M.F., Casavant,T.L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Scheetz,T.E., Brange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McKevan,P.J., Wolley,X.C., Halele,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Worley,X.C., Halele,S., Garcia,A.M., Madan,A., Rodrigues,S., Sanchez,A., Whitingy,M., Madan,A., Rodrigues,S., Shevbenko,Y., Bouffard,G., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Schnerch,A., Schein,J.E., Jones, S.J. and Marra,M.A.

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Brone, M.C., Rodriguez,A.C., Grimwood,J., Smallus,D.E., Brone, M.C., Rodriguez,A.C., Grimwood,J., Smallus,D.E., Brone, M.C., Rodriguez,A.C., Grimwood,J., Smallus,D.E., Brone, M.C., Maral, M.S., Maguer, M.D., Schein,J.E., Jones, S.J. and Marra,M.A.
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      ECUSE324 1639 bp mRNA linear VRT 08-OCT-2003 Danio rerio cDNA clone MGC:65884 IMAGE:6800994, complete cds. BCO56324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg, R.
Direct Submission
Submission
Submitted (11.AUG-2003) Mational Institutes of Health, Mammalian
Submitted (11.AUG-2003) Cancer Genomics Office, Mational Cancer
Gene Collection (MGC), Cancer Genomics Office, Mational Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/mol_type="mRNA"
                                                                                                                            BC056324.1 GI:33604129
                                                                                                                                                                                  Danio rerio (zebrafish)
Danio rerio
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REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

MEDLINE PUBMED

JOURNAL

TITLE

source

FEATURES

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PRI 11-DEC-2002

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BC053205
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Lawrence Berkeley National Laboratory
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley CA 94720
This clone was sequenced as part of a high-throughput process to
This clone was sequence has been subjected to integrity checks
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
Por further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cocha@fruitfly.berkeley.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Elwaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Stapleton, M., Brokstein, P., Hopp, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorset, Hong, L., Agbayani, A., Carlson, J.,
Khunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K.,
Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
Direct Submission
L. Submitted (10-DEC-2001) Berkeley Drosophila Genome Project,
Eavrence Berkeley, CA, 94720, USA
Sequence Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alignment with genomic scaffold AE003639, gene does not completely overlap longest ORF" /db_xref="FLYBASE:FBgn0032484"
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                                                                                                                                     Gaps
                                                                                                                                                                                                                          ;
                                                                                                                                                                                Length 1654;
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Drosophila melanogaster GH27420 full length cDNA.
AY069228
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                                                                                     DB 9; Le.
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                                                                                   1.3%; Score 50; DB 100.0%; Pred. No. 1.8 cive 0; Mismatches
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/protein_id="AAL39373.1"
/db_xref="GI:17861792"
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|strain="y; cn bw sp"
|db_xref="taxon:7227"
|/map="34A10-34A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Longest ORF"
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'gene="CG9431"
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Best Local Similarity 100.0
Matches 50; Conservative
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AY069228
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

(Yprinifornes; Cyprinidae; Danio.

1 (Dases 1 to 1786)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Riansner,R.D., Colling,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Abramson,R.D., Mallek,J.A., Gunaratne,P.H., Richards,S.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Morley,K.C., Hale,S., Garcia,A.M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiling,M., Madan,A., Young,A.C., Shevchenko,Y.,
Butterfield,S.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Butterfield,S.S., Krzywinski,M.I., Skalska,U., Schmutz,J., Myers,R.M.,
Butterfield,S.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Generation and initial analysis of more than 15,000 full-length
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www.shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
/traislation="Werdfy" Granlytppts CHYPLQLRGRIWIEDQPEAFACKPKIV
YPTLSTSINTSKENYTLICRYHGSPRTVIANDYTHOYYESBISKPVKSLQKQRIYIELL
SLIDSKIRTSCHIDVYOKELITUVNARKSDEGYYTCLARNPGGKDSVHISVVVQKDMRRI
SLIDSKIRTSCHIDVAGFLSKNILLFSLYTCLIFRRRKQFHPCQHTYLQPTSLPVQSPG
SERATAISALSSGVIRESKIVLDPLSAINEPSNKNYTLFKTSNSNGSEYMHTRNYKDV
RINSNYYTENDUNQABSISSRNRELYSNIAGDREKBELKQKORLDKOSRYMHTRNYKDV
SRKKQQIDELQPDLLPSTQPTALKNINBTFGPSAKKAEVNBRSKYNTNGQKYLKEKYG
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Submitted (02-UNN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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BC053205
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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100.0%; Pred. No. 1.8e-13;
ative 0; Mismatches 0;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC053205.1 GI:31418862
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Danio rerio
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Landropterygi; Retacas; Chordaea; Craniata; Vertebraea; Euteleostomi; Actinopterygi; Neopterygi; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Dases 1 to 1880)

2 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Riausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Abrangeot,P.P., Range,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Millah,S.J., Gunaratne,P.H., Richards,S., Norley,K.C., Halle,S., Garcia,A.M., Gay,L.J., Hulyk,S.M., Villalon,D.X., Millah,S.J., Garcia,A.M., Garcia,A., Rodrigues,S., Sancher,A., Whiting,M., Madan,A., Young,A., Schwuchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Schwucz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Schein,J.B., Jones,S.J. and Marra,M.A.

Schnerch,A., Schein,J.B., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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NSWPPLSLINHVAHAPPLVVC"
University of Tokyo, Laboratory of Genome Structure Analysis, Hun Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:filodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

WEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' & 3'-end one pass sequencing: Departent of Virology and Human Geneme Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1880 bp mRNA linear VRT 07-OK Danio rerio cDNA clone MGC:56344 IMAGE:5604031, complete cds. BC052972 GI:31418214 MGC.
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                                                                                                                                                                                                                                                                                                                                          1..1820, American appiens" | Organism="Homo sapiens" | Mol Lype="MRNA" | Mol Lype="mRNA" | Mol Xref="taxon:9606" | Colone="HEP11541" | Coll Lype="hepatoma" | Colone lib="HEPE" | ME188FL3" | Mote="cloning vector pME188FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.3%; Score 50; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 50; Conservative 0; Mismatches 0;
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/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 117 Row: 9 Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Unknown (protein for MGC:64021)"
/protein_id="AAH53205.1"
/db_xref="G1:31418863"
/tanslation="MYLSQRGELNRAIADYLRSNGYEEAYSVFKKEAELDMWEELD
KKYAGILEKKWTSVIRLQKKWMELESKLNEAKEEINTGGPIGQKRDPKEWIPRPPEKY
ALSGHRSPVTRVIFHPVFSVIVSASEDATIKVWDHETGDFERTLKGHTDSVQDISFDH
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HVVECISWAPESAHPTILEATGSETKKSGKPQPFLLSGSRDKTIKMDVSIGMCLMTL
VGHDNWVRGYLVHPGGKYIVSCADDKTLRIWDYKNKRCTKTLSAHEHFVTSLDFHKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="COG2319; Region: FOG: WD40 repeat [General function prediction only]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGKLLASCSADMTIKLWDFQGFECIRTMHGHDHNVSSVAIMPNGDHIVSASRDKTIKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
         Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331. .456
/note="LisH; Region: Lissencephaly type-1-like homology
monif"
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Homo sapiens cDNA: FLJ23306 fis, clone HEP11541.
AK026959
                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
/mol type="mRNA"
/db xref="taxon:795"
/dlone="MGC:64021 IMAGE:6793127"
/tissue type="Kidney, zebrafish"
/lone_lib="NCI CGAP_ZKid1"
/lab host="PHIGB"
/note="Vector: pCMV-SPORT6:1"
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Homo sapiens (human)
Homo sapiens
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Pred. No. 1.8e-13;
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100.0%; Pred. No....
0; Mismatches
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VRT 07-OCT-2003

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Contact: MGC help desk
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center (NISC),
Gaithresburg, Maryland;
Naryland,

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/product=="LOC283130 protein"
/protein_id==AAH36869.1"
/db_xref==GI:2247331"
/db_xref="LocusID:283130"
/translation="WYKIYPHESLIGEFKGMSFPIASIAVWSVLFGVYSNTLLVLTA
TSHGRRAQPPSYMH FLAGCTGAYCOAYCLAPPDIJKVRLQNQTEPRAQPGSPPRY
GGYMGCAASIFREEGPRGLPRGAMALTLRDTPTVGIYFITYEGLCRQYTPEGQNPSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R. Direct Submission Direct Submission Submitted (23-AUG-2002) National Institutes of Health, Mammalian Submitted (23-AUG-2002) National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schaefer, C.F., Bhat, N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young, A., Zhang, L.-H. and Green, E.D.
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/organism="Homo sapiens"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbe-remail.nh.gov
Tissue Procurement: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mc@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                           Direct Submission
Submitted (02-UTN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 50; Conservative 0; Mismatches 0; Indels
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/tissue type="Whole body, adult ma
/clone_lib="Sugano SJD adult male"
                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/mol_type="mRNA"
/db_xref="taxon:7955"
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BC036869
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AUTHORS
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Tufan, N.L.S., Lian, Z., Liu, J., Pan, J., Arbuthnot, P., Kew, M., Tufan, N.L.S., Lian, Z., Liu, W. and Feitelson, M.A.
Direct Submission
Submitted (08-FSB-2002) Pathology, Anatomy and Cell Biology, Thomas Jubfitson University, 1020 Locust Street, Philadelphia, PA 19107,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFSELPTPDTPVTPULLCALLLSSDSFLOGETALKNALCOFALPLVLPDSENHYHTF
LLWANRGIVRTWWSQPPRGMGSFREDSVVLSRAPAFAFVRMDVSSNSKSQLLMAVLSP
MEROWDCWRHDLMCTNAREISDGLVBISWPFPSGRREDLDIPPEPVAFUNLRGDIGS
HWLOFKLLTEISSAVPILTDNISKKFYKLLYSMKESTTKYFFILSPYRGKRNYNLRFL
NKLIPPLKTHSHYNYKVSSTDSDSFVKLIRALVGNVLAAPCRRVSVEDMAHAARKLG
LKVDEDCEECQKAKDRWERITRKIKDSDAKTRDELRLOGDPRRKAAQVEKEFFQLQWA
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VIDSGGLIGGALTSAGDRFELEASLATLLMGLSNVTVISLAETKDIPAAILHAFLRLE
KTGHMPNYQFVYQNLHDVSVPGPRPRDKRQLLDPPGDLSRAAAQMEKGGDGFRALAGL
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/podduc_up_regulated gene 4"
/product_uid="AAL83710.1"
/db_xref="di:1922132"
/db_xref="di:1922132"
/db_xref="di:1922132"
/db_xref="di:1928132"
/db_xref="di:19281
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GRLPAGQRRPAHFPGLASELLLTGLPLELIDGSTLSMPVRWYTGLLKELHVRLERRSR
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1 (Bases I to 3806)

1 (Bases I to 3806)

1 (Lian, Z. Liu, J., Pan, J., Arbuthnot, P., Kew, M., Clayton, M.M., Zhu, M. and Feitelson, M.A.

Clayton, M.M., Zhu, M. and Feitelson, M.A.

Geptinis Bx antigen stimulates expression of a novel cellular gene, URG4, that promotes hepatocellular growth and survival
                                                                                                                                                                                                                                                      AYO78404 1inear PRI 27-
Homo sapiens up-regulated gene 4 (URG4) mRNA, complete cds.
AYO78404
                                              organism="Homo sapiens"
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/db_xref="taxon:9606"
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'map="short arm"
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/gene="URG4"
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/gene="URG4"
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/gene="URG4"
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(Loses 1 to 2481)

Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Institute of Generic Resources; 23-1, Toyama

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

1-chome, Shinjuku-ku, Tokyo 162-86410, Japan

1-chome, Shinjuku-ku, Tokyo 162-86410
TVLVAGGFAGIASWVAATPLDVIKSRWQMDGLRRAVYQGMLDCMVSSIRQEGLGVFFR
GVTINSARAFPVNAVTFLSYEYLLRWMG"
704. .979
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                               /note="mito carr; Region: Mitochondrial carrier protein"
/db_xref="CDD:pfam00153"
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Isolation of full-length cDNA clones from macaque brain cDNA
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/clone lib="macaque brain cDNA library QnpA"
/dev_stage="adult"
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1.3%; Score 50; DB 9; Length 2481;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    Length 2275;
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fis (full insert sequence).
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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/organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo.

In (Dases I to 9669; A. Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S. L., Amaratunge, H.C., Burnell, K., Melle, M. Barkar, D. Babbaria, J., Banket, C., Burch, E., Brown, M. Barkar, M. Barkar, D. Babbaria, J., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T. C., Coyle, M. D., Chodhry, I., Christopoulos, C. Chen, Z., Chen, Z., Chiu, D., Chodhry, I., Christopoulos, C. Chen, G., Chen, Z., Chiu, D., Chodhry, I., Christopoulos, C. Chen, G., Chen, M. D., Dathorne, S.R., David, R., David, R., David, M. R., David, M. R., Day-Carroll, L., Dathorne, S.R., David, R., Harande, G., Corell, J., Horat, R., Haris, R., Harande, R., Hollins, R., Han, J., Haris, S., Howard, S., Hubes, S., Horat, R., David, R., Horat, R., Mann, R., David, R., Mann, R., Mann
                                                                                                                                                                                                                    Homo sapiens 12 BAC RP11-324P9 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
AC127894 GI:23307946
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Submitted (19-UUL-2002) Human Genome Sequencing Center, Department
A Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 96967)
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                                                   Gaps
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                                                                                                     Length 3606;
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  1.3%; Score 50; DB 9; Le
Local Similarity 100.0%; Pred. No. 1.7e-13;
tes 50; Conservative 0; Mismatches 0;
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Worley, K.C.
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Homo sapiens
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                                    Best Loci
Matches
                                                                                                                                                                                                                            RESULT 29
AC127894
                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 clones and 2 clones with a minimum of 2 clones and 3 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
ml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Muc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Esports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL;
Worley, K.C.
Direct Submission
Direct Submission
Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 96967)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (28-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                             Department
                                                                                                                                                                                                                                     Direct Submission
Submitted (25-SEP-2002) Human Genome Sequencing Center, Departmer
submitted (25-SEP-2002) Human Genetics, Baylor College of Medicine, One
Pavlor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 25, 2002 this sequence version replaced gi:22380679. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2004 of clone AC139931"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58082, .58416
/standard_name="SHGC-145133"
60409, .60581
/standard_name="SHGC-144174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _name="SHGC-111995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .96967
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db:xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="overlaps bases 1. .'function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1. .2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANNOTATION OF FEATURES:
                                                                                                                                                                                                                                                                                                                                                      Baylor Plaza, Houston,
5 (bases 1 to 96967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Features listing.
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PRI 15-0CT-2002

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Contact: moc usity dues to the formulation of the f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
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Submitted (19-0CT-2002) National Institutes of Health, Mammalian
Gene Collection (WGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
PC C12NS/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,
C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/db_xref="IMAGE:5224224"
/tissue type="Pancreas, Spleen, adult pooled"
/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                            /organism='Homo sapiens (human)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.3%; Score 49; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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Contact: MGC help desk
                                                                                                          EST and encoded human protein
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC038545 444 bp mENA Homo sapiens, clone IMAGE:5224224, mENA. BC038545
                                                                                                                                                                                                                                                                                                                     1. .159
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

    .444
    /organism="Homo sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
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                                                                                                                                                                                                       source
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
BC038545
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COMMENT
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HD121238-1 GI:23216148

HD212238-1 GI:23216148

HD2123216148

HD21233-1 GI:23216148

HD2123216148

HD212316148

HD212148

HD212316148

HD212316148

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HD212316148

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                                      /standard name="RH104171"
91175. .92742
/note="imperfect tandem repeat, confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19,
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                                                                                                                                                                                                                                     94964. .36967
/note="overlaps bases 1. .2004 of clone AC020656"
/function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Unclassified.
Unclassified.
1 (bases 1 to 159)
Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 17182 28-OCT-2003;
Location/Qualifiers
                                                                                                                                                                     map and PCR"
/function="unresolved tandem repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.3%; Score 49; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 7.2e-13;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 50; DB 9; Latity 100.0%; Pred. No. 1.2e-13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR425685 17182 from patent US 6639063. AR425685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AR425685.1 GI:40180795
        .87296
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                    misc_feature
                                                                                                                                                                                                                                                 misc_feature
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source

ORIGIN

PEATURES

AUTHORS TITLE JOURNAL

REFERENCE

LOCUS DEFINITION ACCESSION

RESULT 30 AR425685

à 원 ORGANISM

VERSION KEYWORDS SOURCE

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 31

BD121238

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

390

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ORIGIN

RESULT 33 AX575591/c LOCUS DEFINITION

ACCESSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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unsaction of the project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov
Contact: nisc. mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,K., Stantipop,S., Thourias,P.J., McCloskey,J.C.,
McDowell,J., Pearson,K., Stantipop,S., Thouras,P.J., Tucchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRK plate: 135 Row: K Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16418454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72. 419
70. 199
70. 70 total in Region: Lipocalin / cytosolic fatty-acid binding protein family. Lipocalins are transporters for small hydrophobic molecules, such as lipids, steroid hormones, bilins, and retinoids. Alignment subsumes both the lipocalin and fatty acid binding protein signatures from PROSITE. This is supported on structural and functional grounds. Structure is an eight-stranded beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="mpadlegtwitlssdnpegyvlalgidpatrkiakilkpokvie
ongdsftihtnsslrnyfvkfkvgeefdednrgldnrkckslviwdndrltciokgek
knrgwthwiegdklhlemfcegovckotfora"
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U. Sailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (01-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 1.704
| Organism="Homo sapiens"
| Mol_type="mRNA"
| Ab xref="maxon:9606"
| Clone="MGC:70641 IMAGE:5224517"
| Lissue type="Pancreas, Spleen, adult pooled"
| Clone=lib="NHH MGC_120"
| lab_host="DH10B"
| Note="Vector: pCMV-SPORT6"
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producE=10known (protein for MGC:70641)"
protein id=10kAH63013.1"
/db_xref="GI:38614447"
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1.3%; Score 49; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 6.2e-13;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="CDD:pfam00061"
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                                                                                                                                                                                                                                                                                   Strausberg, R.
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Klausner R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Klausner R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Wax,S.I., Wang,J., Hsieh,F.,
Boatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soaree,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abraman,R.J., Mullay,S.J., Bosak,S.A., McEwan,P.D.,
Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Glbbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodtigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 704)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salceda, S., Macina, R.A., Recipon, H., Cafferkey, R., Sun, Y., Liu, C. and Turner, L.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relating to breast specific genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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1.3%; Score 49; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 6.5e-13;
Matches 49; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.5e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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Diadexus, Inc. (US)
                                          /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX575591 476 bp 1
Sequence 87 from Patent WO02068645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inc. (US)
Location/Qualifiers
             'lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions and methods
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Matches 49; Conservative
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Query Match

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 34 BC063013 LOCUS REFERENCE AUTHORS

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REFERENCE AUTHORS

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To (bases 1 to 959)

Gerards, W.L., Hop, F.W., Hendrike, I.L. and Bloemendal, H.

Cloning and expression of a human pro(tea) some beta-subunit cDNA: a
homologue of the yeat PRS4 subunit essential for
peptidylglutamyl-peptide hydrolase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prosome beta-subunit=multicatalytic proteinase complex [human, ingNA, 959 nt].
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/protein_id="AAB31085.1"
/db_xref="G1:551547"
/trānslation="MDPASALYRGPITRTQNPMVTGTSVLGVKFEGGVVIAADMLGSY
                                                                                          /clone="IMAGE:30291051"
/tissue_type="Jaw and limb, mouse, day 18.5 to new born, pool of mature fore and hind limb, maxilla and mandible containing endochondral and membraneous bone, formed joints, tendon, ligaments, dermis, epidermis, muscle and reeth with newly forming dentin and enamel"
/clone_lib="WIHH MGC_136"
/lab_host="BH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="prosome beta-subunit, HSBpros26"
/note="multicatalytic proteinase complex; yeast
PRE4-subunit homolog; Method: conceptual translation :
partial peptide sequencing; This sequence comes from i; HSBpros26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6013624 GenBank staff at the National Library of Medicine created thi entry (NCBI gibbsq 150354) from the original journal article. This sequence comes from Fig. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2e-13;
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100.0%; Pred. No. 6.2e-13
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV-SPORT6.1"
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94283586
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/db_xref="taxon:9606"
1. 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Homo sapiens
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S71381.1 GI:551546
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecton, M., Soares, M.B., Bonaldo, M.F., Casavatt, T.L.,

Staplecton, M., Soares, M.B., Bonaldo, M.F., Casavatt, T.L.,

Staplecton, M., Soares, M.B., Bosak, S.A., McEwan, P.J.,

Abramson, R.D., Mulahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, T., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

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Butterfield, Y.S., Krzywinski, M., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susmna Onna, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline,
Schein, Duane Smailue, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
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                                                                                                                                                                                                                                                                      ROD 21-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 752)
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Submitted (20-0CT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n and mouse cDNA sequences
Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                             BC060283 752 bp mRNA linear Mus musculus cDNA clone IMAGE:30291051, partial cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            George Yang, Scott Zuyderduyn, Marco Marra.
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Mus musculus
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AUTHORS TITLE JOURNAL

REMARK COMMENT

MEDLINE PUBMED REFERENCE

JOURNAL

TITLE

Euteleostomi,

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GSLARFRNISRIMRVNNSTWLGASGDYADFOYLKOVLGOMVIDEELLGDGHSYSPRAI
HSWLTRAMYSRRSKONPLWNTWVIGGYADGESFLGYVDMLGVAYEAPSLATGYGAYLA
QPLLREVLEKQPVLSQTEARDLVERCMRVLYYRDARSYNRFQTATVTEKGVEIBGPLS
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100.0%; Pred. No. 6e-13;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 49; Conservat
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source

FEATURES

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 37 BC032451 LOCUS

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REFERENCE AUTHORS

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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Rlausner, R.D., Collins, F.S., Wagner, L., Schener, C.M., Schuler, G.D.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwant, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P. H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lux, Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Genen, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Generation and initial naniyals of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="iGv; Region: Immunoglobulin domain variable region (v) subfamily" (db_ref="CDD:cd00099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="IGG; Region: Immunoglobulin domain constant region subfamily" /db_xref="CDD:cd00098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1008)
                                                                                                                                                                                                                                                                                                                 /tissue_type="Brain, Lung, Testis, adult, pooled whole"
/olone_lib="NHH MGC_115"
/lab_host="HH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product=10hknown (protein for MGC:40426)"
/protein_id="AAH12451.1"
/db_xref="GI:21619606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 49; DB 9; Length 997 llarity 100.0%; Pred. No. 6e-13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          'clone="MGC:40426 IMAGE:5178085"

    .997
    /organism="Homo sapiens"

                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3C000761.2 GI:38014219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 49; Conserv
prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC000761
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                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 38
BC000761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Librate 1 (Dates 1 to 291)

Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Poung, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Toucchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.N.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: f Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcombgri.nih.gov/
Contact: nisc_mgcombgri.nih.gov/
Shkhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Yeung,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                       PRI 19-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-UTN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                     HOUJZ451
Homo sapiens cDNA clone MGC:40426 IMAGE:5178085, complete cds.
BC032451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: egapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Employed Springer (M.S.C.)
Sequencing Center (M.S.C.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC032451.1 GI:21619605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bapiens
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

JOURNAL

TITLE

TITLE

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Gaps .

Length 997;

968

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1030)

Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, P.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninof, F., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEvan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.
Worley, K.C., Halele, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Luy, X., Gibbs, R.A.,
Banchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youngh, A.C., Shevhen, E.D.,
Butterfield, Y.S., Rzzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and minial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help deak
Email: cgapbs-remail.nih.gov
Trissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M. AG E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Linn at: http://image.llnl.gov Series: IRAL Plate: 36 Row: b Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7661539
This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="groupmas: CDVIR, MGC4027, CDVI"

/db_xref="LocusID:28981"

/db_xref="MIM:605489"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muscle"
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db xref="taxon:9606"

/clone="INAGE:4293548"

/tissue type="SKeletal Mu

/clone_lib="NIH MGC_81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="CDV-1 protein"
/protein_id="AAH29349.1"
/db_xref="GI:20809377"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="CDV-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1030)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20. ..430

/product="SNARE associated protein snapin"
/product="SNARE associated protein snapin"
/protein_id="AAN00761.1"
/db_xxef="G1:12653935"
/db_xxef="Locuafp:23557"
/translation="WAGAGGAAVSGAGTPVAGPTGRDLFAEGLLEFLRPAVQQLDSHV
HAVRESQVELREQIDNIATELCRINEDQKVALDLDPPVKKLLNNARRRVVLVNNILQNA
QERLRRLNHSVAKETARRRAMLDSGIYPPGSPGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 2 ROW: C Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20070244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC029349 1030 bp mRNA linear PRI 16-SEP-2003 Homo sapiens carnitine deficiency-associated gene expressed in ventricle 1, mRNA (cDNA clone IMAGE:4293548), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                  Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrapa Dy: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
On Oct 28, 2003 this sequence version replaced gi:12653934.
Contact: MGC help desk
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'tissue type="Lung, small cell carcinoma"
'clone lib="NIH MGC 7"
'lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.3%; Score 49; DB 9; Length 100
Best Local Similarity 100.0%; Pred. No. 6e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo mapiens"
| mol_type="mkNA"
| db xref="taxon:9606"
| clone="MGC:2717 IMAGE:2821705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonym: SNAPIN"
/db_xref="LocusID:23557
/db_xref="MIM:607007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="SNAPAP"
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                                                                                         2 (bases 1 to 1008)
Strausberg, R.
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Homo sapiens
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KEYWORDS
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AUTHORS
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BC029349
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Homo sapiens
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BC004905
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.P., Colling, F.S., Wagner, L., Sheamen, C.M., Schuler, G.B.,
Altschul, S.P., Zoeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M., B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullah, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullah, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wazny, D.M., Sodersen, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriques, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                BCUJ8410 1051 bp mRNA linear PRI 06-OCT-2003 Homo sapiens LOC92346, mRNA (cDNA clone MGC:35143 INAGE:5169137), complete cds.
/db_xref="LocusID:28981"
franslation="MIKNLEVQLRRATDEMKAYISSDQQEKRKAIREQYTKNTAEQEN
LGKKLREKQKVIRESHGPINIKQAKWHRDLEQLMECKKQCFLKQQSGTSIGQVIQEGGE
DRLIL"
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1051)
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Direct Submission
Submitted (01-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                      Gaps
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurent: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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                                                                                                                                                                                                                                                                           Length 1030;
                                                                                                                                                           Query Match 1.3%; Score 49; DB 9; Length 103
Best Local Similarity 100.0%; Pred. No. 6e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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BC038410
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PUBMED
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COMMENT
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LTSSKKNWILPILFQVPDVLSKARRNQCDSMLLRNQQLCSTCQEMKNVQPRTRKIPDD
PKASFENCMSYRMSIHQPKGQTTPEPFHDDIPTENIHYRLPILGPRTAVFHGLLTEAY
KTLKERQRSSLPRXEPIGKTTRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1068 bp mRNA linear PRI 16-SEP-2003
Homo sapiens mitochondrial ribosomal protein S2, mRNA (cDNA clone
IMAGE33509565), complete cds.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: b Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21321731. 1.1051
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/db_xref="LocusID:92346"
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1.1%; Score 49; DB 9; Length 1051;
Best Local Similarity 100.0%; Pred. No. 6e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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0, Indels
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                                                                                                                                                                                                                                                                                               db_xref="LocusID:92346"
                                                                                                                                                                                                                                                                                      qene="LOC92346"
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                                                                                                                                                                                                                                                                   .1051
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Gardarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garda, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Marny, D.M., Sodergren, E.J., Lu, X., Gibbe, R.A.,
Fahey, J., Hellen, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, S.S., Karzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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anpedcagfckgenakkriktdekverparthindlenivpflgigllyslsgedlst
alihfrifvgariyhtiayltplpopnrglaffvgygvtlsmayrllrsrlyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is has
in
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John C. Marshall, M.D.; Ph.D
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Contre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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been called MAPEG (Membrane Associated Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/clone="MoC:7269 | MAGE:7269 | MAGE:7269 | MAGE:7269 | MAGE:7269 |
/moce="Woctor: pDNR-LIB"
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/organism="Rattus norvegicus"
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db xref="GI:38649092"
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TITLE
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COMMENT
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GQPTLLGLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: I Row: o Column: 7 This clone has the following problem: The cds is short compared to the longest cds in the locus.
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Status norvegicus cDNA clone MGC:72699 IMAGE:6922267, complete cds.
BC063150
EC063150.1 GI:38649091
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                  2 (bases 1 to 1068)
Strausberg,R.
Strausberg,R.
Submitsed (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                     UIH-MGC Project URL: http://mgc.nci.uih.gov
On Aug 19, 2003 this sequence version replaced gi:13436187.
Ontact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inetitute for Systems Biology
http://www.systemsbiology.org
contact: amadanasystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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1.3%; Score 49; DB 9; Length 1068;
Best Local Similarity 100.0%; Pred. No. 6e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="Brain, neuroblastoma"
/clone lib="NIH MGC 19"
/lab host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1068
/gene="MXPS2"
/note="Synonyms: CGI-91, MRP-S2"
/db_xref="LocusID:51116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3509565"
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                                                                                                                AUTHORS
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Dases 1 to 1320)

2 Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schmaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schoetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McWan, P.J., Peters, G.J., Abramson, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Sanchez, A., Whilting, M., Madan, A., Rodrigues, S., Sanchez, A., Whilting, M., Madan, A., Rodrigues, S., Sanchez, A., Whilting, M., Madan, A., Rodrigues, S., Bukerfield, S., Krzywinski, M.I., Stallaka, U., Schmutz, J., Myers, R., Schein, J. E., Schmutz, J., Myers, R., Schein, J. E., Schmutz, J., Myers, M., Schein, J. E., Schmutz, J., Schmutz, J., Myers, M., Schein, J. E., Schein, J. E., Schwish, J. E., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 121 Row: e Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: nisc mccenhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakealey,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                               HCUS6295 1320 bp mRNA linear VRT 08-OCT-2003
Danio rerio CDNA clone MGC:65806 IMAGE:6792135, complete cds.
BCOS6295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (11-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
CoDA Library Preparation: Invitrogen Corp
CoDA Library Preparation: Invitrogen Corp
CoDA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (MISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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AUTHORS
                                   RESULT 44
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Bicosanoid and Glutathione metabolism). It includes proteins such as Prostaglandin E synthase. This enzyme catalyses the synthasis of PGBZ from PGHZ (produced by cyclooxygenase from arachidonic acid). Because of structural similarities in the active sites of FLAP, LTC4 synthase and PGB synthase, substrates for each enzyme can compete with one another and modulate synthetic activity" /db_xref="CDD:pfam01124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1154)
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Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (06-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 5.9e-13;
rative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 5.9e-13;
ive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5744167"
/clone=Inb=WIH MGC 119"
/lab_host="HH10B"
/note="UH10B"
/note="UH0B"
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Homo sapiens, clone IMAGE:5744167, mRNA.
BC040907
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Matches 49; Conservative
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Matches 49; Conservi
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RESULT 43 BC040907 LOCUS DEFINITION

DRIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL AUTHORS REFERENCE

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FEATURES

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AX587564 1429 bp Sequence 34 from Patent WO0246467.
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Klausher, R.D., Collins, F.S., Wagner, L., Schaefer, C.M., Schuler, G.D.,
Klausher, R.D., Collins, F.S., Wagner, L., Schaefer, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K.D., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morerna, K.D., Mallahy, S.J., Bosk, S.A., McEwan, P.J.,
Norley, K.C., Hale, S., Garzia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Coung, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
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                                                                                                                                                                                                                                                                                               /translation="MGGEDMMSAAEDLADQFLRVTKQYLPHMARLCLISTFLEDGIRM WFOWSEQRDYTEATWSCGYFLATCFVIINLSGOGGGYLVLASNLVOYACFGLFCIIA.
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GRYLLVLMPWTLLHPDSDFFSILQNNVGTALIILVAVGFKTKLAALTLVVWLLAINVY
FNAFWTVPAYKPMHDPLKYDFFQTTSVIGGLLLVVALGPGGVSMDEKKEW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC032932 1346 bp mRNA linear ROD 06-OCT-2003 Mus musculus cDNA clone MGC:41415 IMAGE:1529010, complete cds.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1346)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1320;
                                                                                                                                                                                                 /codon_start=1
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Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             133. .930
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC032932
BC032932.1 GI:21410723
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 67 Row: k Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.

Location/Qualifiers
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Patent: WO 0246467-A 34 13-JUN-2002;
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dfevnvsdarfqamytshlfnldpsdpnfkktkamekileekarhrerkeelliqave
raqqdtgkptqkqpmdpalsmliksvknkteqfqarkkqrv"
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                                                                                                                                                                                                                                                           info@bogsc.bc.co.

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Heilao, Martin Krzywinski, Reta Rutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Sen Lee, Victor Ling, Rana-Liisa Prabhu, Parvaneh Saedi, Jacquellne
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144. .380
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NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
cDNA library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/clone_lib="Soares_mammary_gland_NMLMG"
/lab_höst="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1346;
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| Codon Btatt=1
| Codon Btatt=1
| Product="Unknown (protein for MGC:41415)"
| Protein id="AAH32932.1"
| Ab_xref="GI:21410724"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 49; DB 10; I
100.0%; Pred. No. 5.8e-13;
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Homo sapiens
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FCVHGGLSPSIQTLDQIRTIDRKQEVPHDGPMCDLLMSDPEDTTGWGVSPRGAGYLFG
SDVVAQFNAANDIDMICRAHQLVMGGYKWHFNBTVLTVWSAPNYCYRCGNVAAILELD
                                                                                                                                                                                                                                                                                                                                                     AFU97996 1429 bp mRNA linear PRI 17-DEC-1998
Homo sapiens protein phosphatase X (PPX) mRNA, complete cds.
AF097996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MAEISDLDRQIEQLRRCELIKESEVKALCAKAREILVEESNVQR
VDSPVTVCGDIHGQPYDLKELFRVGGDVPETNYLFMGDFVDRGFYSVETFLLLLALKV
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(Dases 1 to 1429)

Hu, M.C., Tang-Oxley, Q., Qiu, W.R., Wang, Y.P.,

Mihindukulasuriya, K.A., Afshar, R. and Tan, T.H.

Protein phosphatase X interacts with c-Rel and stimulates

G-Rel/fuclear factor kappaB activity

99057922
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/mol_type="unassigned DNA"
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/note="protein phosphatase 4 (formerly x), catalytic subunit (PPP4C) gene."
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (13-OCT-1998) Department of Cell Biology, Amgen, 1
One Amgen Center Road, 14-1-D, Thousand Oaks, CA 91320, USA
Location/Qualifiers
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1.3%; Score 49; DB 9; Length 1429;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          Length 1429
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Hu,M.C.-T., Tang-Oxley,Q., Qiu,W., Wang,Y.-P.,
Mihindukulasuriya,K.A., Afshar,R. and Tan,T.-H.
                                                                                                                                                                                          1.3%; Score 49; DB 6; Le
100.0%; Pred. No. 5.8e-13;
ive 0; Mismatches 0;
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protein_id="AAC96318.1"
db_xref="G1:4028575"
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/mol type="mRNA"
/db_xref="taxon:9606"
1. 1429
                  Location/Qualifiers
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gene="PPX"
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tes 49; Conserv
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AF097996
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74. .1198
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TVPIXEGYALPHAITRIDILAGRDLTDYLMKILTERGVSFTTTAERBIVRDIKELCYV
ALDFREGEMQTAASSSLJEKSPYREDDGQVITIGNBERFCPEALPQPSFLGMESAGIHET
TYNSINKCDADIRKDILAANTVLSGGSTMFPGTAADRWGKEITSLAPPFMKIKXITAPPER
KYSVWIGGSILASLSTFQQMMISKQEYDBSGPSIVHRKCF"
                                                                                                                                                                                      Aiptasia pulchella
Aiptasia pulchella
Aiptasia pulchella
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Aiptasidae, Aiptasia.
B 1 (bases 1 to 1440)
S Lin,C., Tsai,J., Chen,M., Wang,L. and Fang,L.
Characterization of 5'-flanking region of the anemone ATP
ribosylation factor 1 and actin genes
L Unpublished
E 2 (bases 1 to 1440)
S Lin,C., Tsai,J., Chen,M., Wang,L. and Fang,L.
Direct Submission
L Submitted (13-MAY-2003) Research & Planning, National Museum of
Marine Biology & Aquarium, 2 Houwan Road, Checheng, Pintung 944,
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Homo sapiens malonyl-CoA:acyl carrier protein transacylase
(malonyltransferase), mRNA (cDNA clone MGC:47838 IMAGE:6052380),
complete ods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 1499)
Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buctow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heiseh, F.,
Diatchenko, L., Marusina, K., Farmér, A. A., Rubin, G. M., Hong, L.,
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                  INV 01-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="authority: Aiptasia pulchella Carlgren 1943"
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nızy/436
Aiptasia pulchella beta actin mRNA, complete cds.
AY297438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 49; DB 3; L4
Local Similarity 100.0%; Pred. No. 5.8e-13;
Les 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 1440
/organia="Aiptasia pulchella"
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/db_xref="taxon:12924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                            AY297438.1 GI:34148150
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Gaps

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Loudess 1595 bp mRNA linear PRI 11-DEC-2003 Homo sapiens transient receptor potential cation channel, subfamily c, member 4 associated protein, mRNA (cDNA clone IMAGE:3530893), BC008336
                                       LGIENPVCEVSNYLFPDCRVISGHQEALRFLQKNSSKFHFRRTRMLPVSGAFHTRLME
PAVEPLTQALKAVDIKKPLVSVYSNVHGHRYRHPGHIHKLLAQQLVSPVKWBQTWHAI
YERKKGRGFPQTFEVGPGRQLGAILKSCNMQAWKSYSAVDVLQTLEHVDLDPQSPPR"
            LVFAGAMEFAEGLYAVKIRAEAMQEASEAVPSGMLSVLGQPQSKFNFACLEAREHCKS
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gatthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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On Dec 9, 2003 this sequence version replaced gi:14250733.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
                                                                                                                                                                                                                                                                                                                                                                                                                  232. .1128
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S-malonyltransferase [Lipid metabolism]"
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                                                                                                                                                                                                                                                                                                Length 1499;
                                                                                                                                                                                                                                                                                                   Query Match
1.3%; Score 49; DB 9; Length 149;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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Tissue Procurement: ATCC
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Strausberg, R.
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BC008836
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DEFINITION
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SOURCE
ORGANISM
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Contact: MGC help desk
Email: cgapbe_remail.nih.gov
I seue Procurement: ATCC
Tissue Preparation: Life Technologies, Inc.
Tissue Procurement: ATCC
Tissue Preparation: Lissue Tissue Of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hdgafi.nih.gov/
Contact: nisc.mgc@hdgafi.nih.gov/
Contact: nisc.mgc@hdgafi.nih.gov/
Contact: nisc.mgc@hdgafi.nih.gov/
Contact: nisc.mgc@hdgafi.nih.gov/
Akhter.N., Aygle.K., Beckstrom-Sternberg,S.M., Benjamin.B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Haddighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDove,I.G., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsuurgeon,C., Vogt,J.L., Walker,M.A.,
Young,A., Zhang,L.-H. and Green,E.D.
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, K., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanobez, A., Whiting, M., Madan, A., Young, J.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAH42195.1"
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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.inh.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Souffard,G.G., Breen,K., Brinkley,C.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., No.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantins,E., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantipop,S., Thorbas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green, B.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
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AGTYLCILEKFFPDIIKIHWQEKKSNTILGSQEGNTMKTNDTYMKFSWLTVPEESLDK
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DTLLLQLINTSAYYTYLLLLKSVVYFAIITCCLLRRTAFCCNGEKS"
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Villalon, D.K., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.L., Skalska, U., Smailus, D.E., Schnerzhion and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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/note="IGC; Region: Immunoglobulin domain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg,R.

Direct Submission
Submitted (12-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284. 592
/note="IGV; Region: Immunoglobulin domain variable
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                                                                                                                                                                                                                                                                           TITLE
      Contact: nisc mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakealey, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakealey, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Hansen, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masfello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tinelation="Qreavespirgtrsyadomfilkrgllehilycivdsecksrdv
losyfdlicelmkrwdafkrenkvintdakroyfikginselvdsmukrcytlsld
froydmkvaevlescklilayisqvptomsfilhilithyciltomvsclntslv
ilmlarrkreilpivtrilomehskkrypgillinnfhulrrwoohylhkdsstcen
sccisfsywketvsiilnpdrospsalvsyieepymdidrdfee"
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Straubberg.R.D., Collins, F.S., Wagner, L. Shemmen, C.M., Schuler, G.D.,
Altachul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Blatchenko, L., Marushina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Azaninci, P., Prasnge, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                            be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonyms: DKFZP727M231, DKFZp586C1223, dJ756N5.2,
FRRP4AP, C2Oorf188, TRUSS"
/db_xref="LocusID:26133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1655)
                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 20 Row: a Column: 9.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC039725 119-NOV
Homo sapiens cDNA clone MGC:47828 IMAGE:5227869, complete cds.
BC039725
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100.0%; Pred. No. 5.7e-13;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Muscle, rhabdomyosarcoma"
/clone lib="NIH MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="TRPC4AP protein"
/protein_id="AAH08836.2"
/db_xref="GI:39645211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="LocusID:26133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3530893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="TRPC4AP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="TRPC4AP"
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BC039725.1 GI:24980796
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Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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BC039725
LOCUS
DEFINITION
ACCESSION
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VERSION
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                         FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haish, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninoi, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.C., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whilting, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whilting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                        LCU25753 1661 bp mRNA linear PRI 12-NOV-2003
Homo sapiens myozenin 1, mRNA (cDNA clone MGC:34233 IMAGE:5202455),
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Akhter.N., Ayole.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dierrich,N.L., Granite,S., Guan,X., Gupta,J., Hadhighi,P.,
Mansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: egapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                                            Length 1655;
                                                                                                   Score 49; DB 9; Le
Pred. No. 5.7e-13;
                                                                            1.3%; Scott
100.0%; Pred. No.
subfamily"
/db_xref="CDD:cd00098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC025753.1 GI:19343990
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                                                                                                                         l Similarity 100.
49; Conservative
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                                                                                                        Query Match
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JOURNAL
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AUTHORS
                                                                                                                                                         Matches
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BC025753
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AUTHORS
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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KEYWORDS
SOURCE
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COMMENT
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John This family consists of several mammalian (Calsarcin). This family consists of several mammalian (Calsarcin). This family consists of several mammalian (Calcineurin-binding proteins. The calcium- and calcineurin-binding proteins. The calcium- and calmodulin-dependent protein phosphatese calcineurin has been implicated in the transduction of signals that control the hypertophy of cardiac muscle and slow fibre gene expression in skeletal muscle. Calsarcin-1 and calsarcin-2 are expressed in developing cardiac and skeletal muscle during embryogenesis, but calsarcin-1 is expressed specifically in adult cardiac and slow-twitch skeletal muscle, whereas calsarcin-2 is restricted to fast skeletal muscle. Calsarcins represent a novel family of sarcomeric proteins that link calcineurin with the contractile apparatus, thereby potentially coupling muscle contractile apparatus, thereby potentially coupling muscle expressed specifically in skeletal muscle and is enriched in fast-twitch muscle fibres. Like calsarcin-3, and calsarcin-2, calsarcin-3 interacts with calcineurin, and calsarcin-2, calsarcin-3 interacts with calcineurin, and calsarcin-2 are calcineurin, gamma-filamin, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPLSGTPAPNKRRSSKLIMELTGGGGESSGLNLGKKISVPRDV
MLEELSLLTRRGSKWFKLRQMRVBKFIYBNHPDVFSDSSMPHPQKFLPTVGGQLGTAG
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GVGEYGSGDQAGGSCKHIYVFRTY1SPWERAMGVDPQQXMELGIDLLAYGAKABLBKY
KSFNRTAMPYGGYEKASKRMTFQMPKFDLGPLLSEPLVLYNQNLSNRPSFNRTPIPWL
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                                                                                          clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 49 Row: d Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21359948.
Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'tissue type="Lung, Spleen, fetal, pooled"
'clone lib="NIH MGC 122"
'lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _note="synonyms: FAIZ, CS-2, MYOZ"

db_xxef="LocusID:58529"

db_xxef="MIM:605603"
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ilarity 100.0%; Pred. No. 5.7e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="MGC:34233 IMAGE:5202455"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pCMV-SPORT6"
                                    Young, A., Zhang, L.-H. and Green, E.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/db xref="CDD:pfam05556"
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                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="MYOZ1"
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us-10-005-907-1.oligo.rge

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Location/Qualifiers
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Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    analysis.
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AK112205
LOCUS
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausherr, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausherr, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhar, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Wans, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.H., McZwan, P.J.,

McKernan, K.J., Male, Y.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,

Generation and mouse cDNA sequences

L. Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC035953 1687 bp mRNA linear ROD 06-OCT-2003
Mus musculus RIKEN cDNA 3010015K02 gene, mRNA (cDNA clone MGC:31682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1687)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (31-7UL-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                     Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 3926 14-JUN-2001,
Millennium Predictive Medicine, Inc. (US)
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 49; DB 6; Le
Local Similarity 100.0%; Pred. No. 5.7e-13;
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  AX188231.1 GI:15139704
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                                                     Homo sapiens (human)
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Matches
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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FLI_CDNA.
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xrefe="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK112205
Ciona intestinalis CDNA, clone:ciad007m12, full insert sequence.
                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/JLNL at: http://image.llnl.gov Series: IRAK Plate: 44 Row: k Column: 18. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 5.7e-13;
tive 0; Mismatches 0;
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MEDLINE
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ECUG1980 11-DEC-2003
Rattus norvegicus CDNA clone MGC:72261 IMAGE:5597975, complete cds.
BC061980
                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Sexies: IRAK Plate: 21 Row: h Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                   Sequencing Center
Center code: BM-HGSC
Web site: http://www.ngsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunazarne, PH., Garcia, A.M., Iu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Strausberg, R.L., Felngold, B.A., Grouse, L.H., Derge, J.G.,
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Best Local Similarity 100.0%; Pred. No. 5.7e-13;
Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STFQQMWISKQEYDESGPSIVHRKCF"
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Rattus norvegicus
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Procurement: DCTD/DTP
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Boronstein, M.J., Gasmant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                        2 (bases 1 to 1706)
Satou Y. and Satoh, N.
Direct Submission
Direct Submission
Submitted (04-0CT-2002) Nori Satoh, Kyoto University, Department of
Zoology; Sxyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail:satoh@ascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095,
Pax:81-75-705-1113)
Ciona intestinalis CDNA Project (URL:
http://ghost.zool.kyoto-u.ac.jp/indexrl.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bcuizes4 1729 bp mRNA linear PRI 03-OCT-2003
Homo sapiens actin, beta, mRNA (cDNA clone MGC:9832 IMAGE:3863361),
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1729)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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100.0%; Pred. No. 5.7e-13;
tive 0; Mismatches 0;
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/organism="Ciona intestinalis"
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/clone="ciad007m12"
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CONtact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov
Contact: nisc mg@cmhgrin.nih.gov
Contact: nisc mg@cmhgrin.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.M., Bouffand,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Cuan,X., Gupta,J., Hadpinghi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                     Altschul, S.F., Zeeberg, B., More, T., Max, S.I., Wang, J., Haich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Wang, J., Haich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Wubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, F.L., Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M.W., Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smallus, D.E., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, Y.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 137 Row: b Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31377483. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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/tissue type="rrestate, pool of NCI_CGAP_Pr30, 40, 41 and
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DALDKIKTKGKGAPFNHFDPSCLFPACRDYWTYHGSFTTPPCEECIVWLLLKEPMTVS
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R.
Direct Submission
Submitted (10-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/protein_id="AAH61980.1"
db_xref="GI:38541366"
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Calone_lib="NCI_CGAP_Pr49"

Abb host="DH10B"

/note="Vector: pcMV-SPORT6.1"
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Vector:

Vector:

National Maria Cardynords

R. Site2:
DrallI (CACCATGTG)

Description: Ist strand orDNA was synthesized considered to the product was digested with Sfil and size selection was performed to using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments 4.1.5kb.The Sfil and size selection was performed to the DrallI sites of pME185-FL3. Khol sites just outside the DrallI sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., University of Tokyo, Institute of Medical for sequencing (5' end primer [CGACCTGCAGGTGGGG];

Science). Custom primer used for sequencing (5' end primer [CGACCTGCAGGTGGAGCAG]).

Location/Qualifiers
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Isolation of novel full-length cDNA clones from macaque testis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB070107 1786 bp mRNA linear PRI 16-AUG-2001 Macaca fascicularis testis CDNA clone:QtsA-14034, full insert
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2 (bases 1 to 1786)

Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.

Direct Submission

Direct Submission

Infectious Diseases, Division of Genetic Resources; 23-1, Toyama

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

Temail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
Tel:81-3-5288-11181)

ToP10

ToP10
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AB070107.1 GI:15208054
oligo capping; fis (full insert sequence).
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
58 . 819
/note="carb_anhydrase; Region: Eukaryotic-type carbonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hashimoto, K., Osada, N., Hida, M., Kusuda, J., Tanuma, R., Hirai, M.,
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/clone_lib="macaque testis cDNA library QtsA"
dev_sigge="adult"
                                                                                                                                                                                                               Length 1737;
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1.3%; Score 49; DB 10; L
Best Local Similarity 100.0%; Pred. No. 5.7e-13;
Matches 49; Conservative 0; Mismatches 0;
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/protein_id="BAB63052.1"
                                                                anhydrase" // db_xref="CDD:pfam00194"
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Homo sapiens
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Best Local Similarity
Matches 49; Conserv
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                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This close was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuracily this particular cDNA clone. However, there artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="AT09813p"
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Fpytspslamvilqdpqdvprgrmlqtikhisellreavedqthg"
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                               INV 15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarain, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
                                                                                                                                                                                                 .
0
                                                                                                             Length 1786;
                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                            AY118452 1806 bp mRNA linear Drosophila melanogaster AT09813 full insert cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Drosophila melanogaster"
                                                                                                     Score 49; DB 9; L
Pred. No. 5.7e-13;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CG7804"
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341. .1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
'db xref="GI:15208055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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L. .1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cdna@fruitfly.berkeley.edu.
Location/Qualifiers
1. .1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Longest ORF"
                                                                                       1.3%; Scor
100.0%; Pred
0; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                AY118452.1 GI:21428321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                  Similarity
                                                                                                                                                        49;
                                                                                                               Query Match
                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                            LOCUS
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                              RESULT 59
AY118452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                 ORIGIN
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Longers 1 Colling. F.S., Wagner, L.H., Derge, J.G.,

Klausner, R.D., Colling. F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Klausner, R.D., Colling. F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, W. B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Morley, K.C., Hale, S., Garda, A.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Belton, R., Ketteman, M., Madan, A., Rodriques, S.,

Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sharlus, D.E.,

Schnerch, A., Schein, J. E., Jones, S.J. and Marra, M.B.

Generation and Initial analysis of more than 15,000 full-length
                           HLRCFDLIVLGLSYNTTBQDLREYFETYGDVVKAEIKKDTRSGHSKGFGFVRFGSYDV
QWYLJSKHBFIDGRWCEVYFDARGMONGPEGKFVVGRCTBDIBADDLREYFSKFGEV
IDVET FREPRARSFYFLDPYVPRVVCGRKHIIKGYSVHVSTADKKKVQNKNQLFQTN
NYNNLDNNFKNOPANNFRMHPANNFSMHSFNPGYQMKVMN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC029874 1inear PRI 07-OCT-2003
Homo sapiens protein inhibitor of activated STAT protein PIASY,
mRNA (CDNA clone MGC:35296 IMAGE:5176540), complete cds.
VDTKAVRGVRSNEGRLYSPSEETGWGEYHYFCVFPKKNKRQSEDNLENSTAKTKRTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1835)
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Direct Submission
Submitted (16-MAY-2002) National Institutes of Health, Mammalian
Submitted (16-MAY-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, I.Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH. MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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0
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                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                       Score 49; DB 3; Le
Pred. No. 5.7e-13;
                                                                                                                                                                                                                           1.3%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
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BC029874.1 GI:20987516
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                                                                                                                                                                                                                                                                                                                             Conservative
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Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Habeh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Wullahy, S.G., Guararne, P.H., Richards, S.,
Moren, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, K., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodingues, S.,
Sanchez, A., Whiting, M., Madn, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 143 Row: g Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Silurana tropicalis"
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KVDLSNPEYTVIVEIIKNVCCFSVVKDYTVFRKYNLQEVIKSSKEEKPQQPTKEDKEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg,R.

Direct Submission
Submission
Submisted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                             245491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                      PUBMED
REFERENCE
AUTHORS
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PUBMED
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COMMENT
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SAP; Region: Putative DNA-binding (bihelical) motif predicted to be involved in chromosomal organisation" /db_xref="CDD:smart00513"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC061320 1R38 bp mRNA linear VRT 04-NOV-2003 Silurana tropicalis cDNA clone MGC:75804 IMAGE:5382264, complete
                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: m Column: 22.
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VPCRAETCAHLQCFDAVFYLQMNEKKPTWMCPVCDKRAPYDQLIIDGLLSKILSECED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVQFDCS PELFKKI KELY ETRYAKKNS EPAPQPHR PLDPLTMES TYDRAGAVPRT PLA
GPNI DY PVLYGKYLNGLGRL PAKTI KPEVRLVKL PPFNMLDBILLKPTELVPQNNEKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPCI FALTPRQVEL IRNSRELQPGVKAVQVVLRI CYSDTSCPQEDQYPPNI AVKVNH
SYCSVPGYYPSNKPGVEPKRPCRPI NLTHLMYLSSATNRI TVTWGNYGKSYSVALYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADELEYLVDGSWCPIRAEKERSCSPQGAILVLGPSDANGLLPAPSVNGSGALGSTGGG
GPVGSMENGKPGADVVDLTLDSSSSSEDEEEEEEEEEDEDEEGPRPKRCPFQKGLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clifton, S.W.
                                                                                                                                                                           /organism="Homo sapiens"
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|mol type="makna"|
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|lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon start=1
'product="protein inhibitor of activated STAT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1838)
Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J.,
and Richardson, P.
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Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                             note ... Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="synonym: MGC35296"
db_xref="LocusID:51588"
db_xref="MIM:605989"
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BC061320
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DME18S-FL3 (Acc.No. AB009864)
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AB063046
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zoedan, H., Moore, T., Wax, S.I., Wang, J., Haieh, F.,
Boatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casvant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninoi, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,
Abramson, R.D., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.C., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Halele, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whilting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, S.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1850)
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Direct Submission
Direct Submission
Submitted (23-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1.3%; Score 49; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 49; Conservative 0; Mismatches 0;
NLXETQGTQNTAHS'
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/mol type="mRNN" | /db_xref="taxon:9606" | /db_xref="taxon:9606" | /dlone="IMAGE:5190011" | /tissue type="Colon, Kidney, Stomach, adult, whole pooled" | /clone_lib="NIH MGC_116" | /cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Unknown (protein for IMAGE:5190011)"
/product="Unknown (protein for IMAGE:5190011)"
/protein id="AAH44318.1"
/bx xete="GI:27924314"
/translation="WAVSSEHFVSALTVFINSKSLSSIKIEDTPVDDPSLKILVANNS
DTLRILKMSSCPHVSSDDGLHFLKLE"
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2 (bases 1 to 1894)

Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.

Direct Submission

Direct Submission

Infectious Diseases, Division of Genetic Resources; 23-1, Toyama

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)

Toble

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Macaca fascicularis brain cDNA clone:@moA-11972, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Helao, Martin Krzywinski, Reta Kutsche, Oliver Les Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danne Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 87 Row: j Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16306585 This clone has the following problem: The cds is short compared to the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB063046.1 GI:14388491 oligo capping; fis (full insert sequence).
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catárrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Isolation of full-length cDNA clones from macaque brain cDNA
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1 Similarity 100.0%; Pred. No. 5.6e-13;
49; Conservative 0; Mismatches 0;
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1. .1850
/organism="Homo sapiens"
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/gene="SAP-1"
150. 1445
/gene="SAP-1"
150. 1445
/gene="SAP-1"
/note="Homology region A with Elk-1 protein (Ets domain)
/note="Homology region A with Elk-1 protein (Ets domain)
is bp 150-417, amino acids 1-89; Homology region B with
Elk-1 protein, required for cooperative ternary complex
formation with Sap is bp 565-617, amino acids 136-157;
Sequence diverges from SAP-1B at bp 1229, amino acid 360;
Homology region C with Elk-1 protein, core of regulated
transcription activation domain, is bp 1203-1355, amino
acids 35-402, (S/T)P motifs conserved between SAP-1A and
Elk-1 are located at amino acids T354, T361, T366, S381,
S387, T420, S425, corresponding to bp 1209-1214, bp
120-1215, bp 1245-1250, bp 1290-12155, bp 1308-1313, bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (05-MAR-1992) Richard Treisman, Transcription Laboratory,
Imperial Cancer Research Fund, London, England
ON Nov 29, 1993 this sequence version replaced gi:338036.
Original source text: Homo sapiens CDNA to mRNA.
Location/Qualifiers
                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element Cell 68 (3), 597-612 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMSAFIA / REPORT 1933 bp mRNA linear PRI 17-DEC-1. Homo appiens / SRF accessory protein 1A (SAP-1) mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                       Bull,J.H., Ellison,G. and Paskins,L.D.
Diagnostic methods for the detection of prostate disorders
Patent: WO 0136674-A 20 25-MAY-2001;
AstraZeneca AB (SE)
Location/Qualifiers
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1.3%; Score 49; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 49; Conservative 0; Mismatches 0;
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Homo sapiens (human)
                                                                                                                                                                                                      1. .1933
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo Bapiens"
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/db_xref="taxon:9606"
1. .1933
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Dalton, S. and Treisman, R.
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           Homo sapiens
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R. Sitel: DrailI (CACTGTGTG)

R. Site2: DrailI (CACCATGTG)

Description: 1st strand cDNA sprimed with an oligo(dT) primer farged corpution: 1st strand cDNA beas primed cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments 41.5kb.The Sfil and size selection was performed to exclude fragments 41.5kb.The Sfil digested PCR product was cloned into distinct DrailI sites of pME18S-F13. XhoI sites just outside the DailII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of
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/clone_lib="macaque_brain_cDNA_library_QmcA"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1933;
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100.0%; Pred. No. 5.6e-13;
tive 0; Mismatches 0;
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Pred. No. 5.6e-13;
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Patent: US 6537811-A 3 25-MAR-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           1. .1894
/organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xxef="taxon:9541"
/clone="QmoA-11972"
                                                                                                                                                                                                                                                                           Custom primer used for sequencing ( 5, end primer [CGACCTGGACATGGACACACACACA] ).

Location/Qualifiers
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100.0%; Pred. No. 5.
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/wol_type="genomic DNA"
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Freier, S.M.
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Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 49; Conservat
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL REFERENCE AUTHORS

ORIGIN

DEFINITION

LOCUS

RESULT 64 AR300635

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FEATURES

ORIGIN

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 65 AX146886 LOCUS

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Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyrrinidae; Danio.

I (Dases 1 to 1940)

S trausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Alaschul, S.F., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Ioquellano, N.A., Peters, G.J.,
McKernan, K.J., Mullahy, S.J., Boask, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Brookers, T. R. Sone, Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                    /translation="mdsAITLMQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARL
WGIRKNKPNMNYDKLSRALRYYYVKNIIKKVNGQKFVYKFVSYPEILNMDPMTVGRIE
GDCESLNFSEVSSSKDVENGGKDKPPQPGAKTSSRNDYIHSGLYSSFTLNSLNSSNV
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Submitted (15-MUG-2003) National Institutes of Health, Mammalian
Submitted (15-MUG-2003) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCO56597 1940 bp mRNA linear VRT 08-00 Danio rerio cDNA clone MGC:65863 IMAGE:6800154, complete cds BCO56597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: egapba-r@mail.nih.gov
Tissue Procurement: Dr. Chi-bin Chien
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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Matches 49; Conserv
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 121 Row: n Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but, not identity to protein.
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Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Hansen,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ab_xref="CDD.pfam03957"
948. .1139
//note="bzIP; Region: bzIP transcription factor. The Pfam
entry includes the basic region and the leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1970)
Strausberg,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282. .923 // Indee="UNK; Region: Jun-like transcription factor. The c-Jun Wh(2)-terminal kinase (JNK) is a member of an evolutionarily conserved sub-family of mitogen-activated protein (MAP) kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1940

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="MGC:65863 IMAGE:6800154"

/clone Tibe="NGC:65863 IMAGE:6800154"

/clone Tibe="NGC:65863 IMAGE:6800154"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6.1"
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100.0%; Pred. No. 5.6e-13;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1970 bp mRNA
Homo sapiens, clone IMAGE:5202626, mRNA.
BC051026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region"
/db_xref="CDD:pfam00170"
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Homo sapiens
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R. Site: pMEIRS-FL3 (Acc.No. AB009864)
R. Site: DraIII (CACGATGTG)
Description: 1st strand clow, was primed with an oligo (dT) primer Description: 1st strand clow, was primed constructed was synthesized using specific 5' and 3' primers and amplified by PGR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.8kb.The Sfill-digested PCR product was cloned into distinct DraIII sites of pWEISS-FU3. XhoI sites just outside the praIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., Institute of Medical Science, University of
Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan Email:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stegomyia.

1 (bases 442 to 1971)

1 (bases 442 to 1971)

Aeder asen,B.T. Severson,D.W. and Christensen,B.M.

Aedes aegypti: characterization of a hemolymph polypeptide expressed during melanotic encapsulation of filarial worms

Exp. Parasitol. 79, 313-321 (1994)

2 (bases 1 to 2015)

Yoshiga,T., Hernandez,V.P., Fallon,A.M. and Law,J.H.

Mosquito transferrin, an acute-phase protein that is up-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-AUG-1997) Biochemistry, University of Arizona,
Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 upon infection
Proc. Natl. Acad. Sci. U.S.A. 94 (23), 12337-12342 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aedes aegypti transferrin precursor, mRNA, complete cds. AF019117
AF019117.1 GI:2645496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="temporal lobe right"
/clone_lib="macaque brain cDNA library QtrA"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OB 9; here,
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    1988
/organism="Macaca fascicularis"

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Aedes aegypti
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1.3*; Score 49; DB
Best Local Similarity 100.0*; Pred. No. 5.6
Matches 49; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9541"
/clone="QtrA-10930"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshiga, T
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AF019117
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                                                                                                     VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-rafmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
DNA Library Preparation: Life Technologies, Inc.
DNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Dy: National Institutes of Health Intramural
Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C.,
Blakesley,R.M., Douffard,G.G., Maren,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Macaca fascicularis brain cDNA clone:QtrA-10930, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  through the I.M.A.G.E. Consortium/Linn at: http://image.llnl.gov
Series: IRAK Plate: 93 Row: i Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene
prediction.
           Submitted (11-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele:
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
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/tissue type="Lung, Spleen, fetal, pooled"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1970;
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Olgo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3%; Score 49; DB 9; L. Best Local Similarity 100.0%; Pred. No. 5.6e-13; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6"
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Gaps

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INV 27-NOV-1997

94305

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 117 Row: i Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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Abedinia,M., Layfield,R., Jones,S.M., Nixon,P.F. and Mattick,J.S. Nucleotide and predicted amino acid sequence of a cDNA clone encoding part of human transketolase
                                                                                                                                                                                                                                                                                                                                                                                                NUH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Mail: egapbs-rémail.nih.gov
Tissue procurement: Leonard I. Zon, M.D.
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Dy: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943'
Web Site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) medspaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                        Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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1.3%; Score 49; DB 5; Length 203:
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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Human transketolase (TKT) mRNA, complete cds.
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/tissue_type="Xidney, zebrafish"
/clone_lib="NGC:CGAP_ZXid1"
/lab_hose="DH10B"
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U55017.1 GI:1297296
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                                                                                                                                                        2 (bases 1 to 2031)
Strausberg, R.
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LOCUS
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COMMENT
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1 (bases 1 c. 2031)

2 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeberger, B., Magner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeberg, B., Mancor, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K.P., Farnage, T.P., Ranae, T.L., Schaefer, C.F., Bhat, N.K., Bohatchenko, L., Marusina, K.P., Farnage, T.P., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Walley, J.A., Gunaratne, P.H., Richards, S., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A., Bouffard, G.G., Blakesley, R.M., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M., Human and Marra, M.B.
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LCEDSCYRPFTTGPACSWAQRPWGSYNGDINSKYPGLLGGYGYDAKUSAYDDKA
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LATDSBLSPLEKBLKGLSDLFGSACLVGKYSPNDEVNRLLKKRRYSNLCALCERPEVCD
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BC053219.1 GI:31419505
MGC.
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5.6e-13;
0; Indels
                                                                                                                                                                                    /db_xref="taxxn:7159"

tissue_type="whole body"

/dev_stage="larva"

4. 1905

4. 1005

/function="iron-binding protein"

/function="iron-transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 1.3%; Score 49; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.6e-13
Matches 49; Conservative 0; Mismatches 0
                                                                                        organism="Aedes aegypti"
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/product="transferrin"
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                                                                                                                    mol_type="mRNA"
strain="Rockefeller"
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GVATEKAVELAAUTKGICFIRTSRPENAIIYNNEDFQVGGAKVULKSCDQVVTIGA
GVTLHEALAAAELLKKEKINIRVLDPFTIRPLDRKLILDSARATKGRILTVEDHYYEG
GIGBAVSSAVVGEBGITVTHLAVNRVPRSGKPAELLKMFGIDRDAIAQAVRGLITKA"
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ISSDLDGHPVPKQAFTDVATGSLGQGLGAACGMAYTGKYFDKASYRVYCLLGDGELSE
GSVWEAMAFASIYKLDNLVAILDINRLGQSDFAPLQHQMDIYQKRCEAFGWHAIIVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSYBELCKAFGQAKHOPTALIAKTFKORĞITGYEDKEĞNHGKPIPKONMAEQI1OBIYS
QIQSKKKILATPPQEDAPSYDIANIRMPSLPSYKYGDKIATRKAYGQALAKLGHASDR
IIALDGDTKNSTFSEIFKKEHPDRFIECYIAEQNMYSIAVGCATRNRTYPFCSTFAAF
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Abedinia, M., Layfield, R., Jones, S.M., Nixon, P.F. and Mattick, J.S. Nucleotide and predicted amino acid sequence of a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abedinia, M., Layfield, R., Jones, S.M., Nixon, P.F. and Mattick, J.S. Widleotide and predicted amino acid sequence of a cDNA clone encoding part of human transketolase Biochem. Blochwe. Res. Commun. 183 (3), 1159-1166 (1992)
                                             2 (bases 1 to 2038)
Schenk, G., Layfield, R., Candy, J.M., Duggleby, R.G. and Nixon, P.F.
Molecular evolutionary analysis of the thiamin-dependent enzyme,
transketolase
                                                                                                                         Unpublished

Joses 1 to 2038)

Schenk, G., Candy, J.M., Duggleby, R.G. and Nixon, P.F.

Direct Submission

Submitted (186-MAR-1996) G. Schenk, Biochemistry, University of Queensland, Brisbane, Qld 4072, Australia

On May 6, 1996 this sequence version replaced gi:339941.
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Biophys. Res. Commun. 183 (3), 1159-1166 (1992)
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Local Similarity 100.0%; Pred. No. 5.6e-13; les 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="transketolase"
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                                                                                                                                                                                                                                                                                 1. .2038
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1. .1872
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transketolase.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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Matches
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HSTRANSK
                                 PUBMED
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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JOURNAL
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FEATURES
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GIOSKKKLIATPPQEDAPSVOIANIRMSLPSYKGƏKIATAKAYĞYĞALAKGHSABR
GIOSKKKLIATPPQOIANAKIGERPPRETECY TABONNYSIAVGCATRNETVPFRYPT
FTRAPOOIRWAAISENINLGGSHCGVSIGEDGASQWALEDLAMFRSYPTSYPSYP
GVATEKAPTAANIKGICFIRTSREPRANIIYNDEDRQYGGAKTVLKSYODQYYTGK
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GYTLAHBALAAABLLIKKEKINIRVLDPFIIKELDRKIILDSARATKGRILTVBBHYYB
GIGBAVSSAVVGEPGITVTHLAVNRVPRSGKPAELLKMFGIDRDAIAQAVGLITKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRT 03-DEC-2003
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ISSDLDGHPVPKQAFTDVATGSLGQGLGAACGMAYTGKYFDKASYRVYCLLGDGELSE
GSVWEAMAFASIYKLDNLVAILDINRLGQSDPAPLQHQMDIYQKRCEAFGWHAIIVDG
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                                                                                                                                                   9419340

3 (bases 1 to 2104)

3 (bases 1 to 2104)

Singleton, C. K.

Singleton, C. K.

Submitted (11-AUG-1992) C. K. Singleton, Vanderbilt University, Box

Submitted (11-AUG-1992) C. K. Singleton, Vanderbilt University, Box

Submitted (11-AUG-1992) C. K. Singleton, Vanderbilt University, Box

Location B, Nashville, TN 37235, USA

Location/Qualifiers
Cloning of human transketolase cDNAs and comparison of the nucleotide sequence of the coding region in Wernicke-Korsakoff and non-Wernicke-Korsakoff individuals
J. Biol. Chem. 268 (2), 1397-1404 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC063356
Silurana tropicalis cDNA clone MGC:75895 IMAGE:5383371, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (passes 1 to 2177)
Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                      1. .2106
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/clone="pTKa-1, pTKd-1"
/tissue type="frontal cortex, liver"
/clone_lib="frontal cortex and liver cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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1.3%; Score 49; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silurana tropicalis (Xenopus tropicalis)
Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71. .1942
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BC063356.1 GI:38648981
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us-10-005-907-1.oligo.rge

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ESM Mus musculus (Craniata, Vertebrata, Euteleostomi, Mus musculus (Craniata, Craniata, Vertebrata, Euteleostomi, Musculus Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 2182)

1 (bases 1 to 2182)

2 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Riausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soarse, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninol, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Norley, K.C., Halle, S., Garcia, A.M., Madan, A., Rodrigues, S., Sanchez, A., Whiling, M., Madan, A., Rodrigues, S., Shevchen, E.D., Dickson, M.C., Butkesley, R.W., Touchman, J.W., Garcia, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E., Schnerch, A., Schein, J.E., and Marza, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BUUZ/124 1600 21-0CT-2003
Mus musculus hypothetical protein LOC217820, mRNA (cDNA clone
IMAGE:4953665), partial cds.
   SVDGTLLALKNLCISSGAALPAILMDTSYAVSSHWKLFTGQVSSPIDCVMCYGPLVPD
GYSVCFAPSLDSITVCVSAFDCCQETDAQKLSDSLQGALRDMQSLIIKCQPGEA"
180. .1925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: angobcm.tmc.ed
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk femal: gapbs.remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                        /note="Carn_acyltransf; Region: Choline/Carnitine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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                                                                                                                                                                                                                                                                             Length 2177;
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                                                                                                                                                                                                                                                                          Query Match
1.3%; Score 49; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                            o-acyltransferase"
/db_xref="CDD:pfam00755"
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Strausberg, R.
Direct Submission
                                                                               misc feature
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KEYWORDS
SOURCE
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JOURNAL
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BC027154
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COMMENT
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altachner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Habeh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.,
Villalon, D.K., Wuzny, S.J., Bosak, S.A., McEwan, P.J.,
Villalon, D.K., Wuzny, D.M., Sodargren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Mund and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at: http://image.llnl.gov Series: IRAK Plate: 143 Row: j Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="Embryo, Silurana tropicalis, neurula (stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OHOOMI-FLANDSYKTOREPVOYLTTHRNSWGRAYTTLIRDRINKESVRSIORTET
VCLDATALKYSEELYSSRTAAQMLHGGGTHANSGNRRFDKTLOFVVGEDGTGGLIYDO
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PHOYNDPFGSCREPGYKRDKVLLOPAHKSLSOYTVCKNYGFRQMDVINSDGSPLTBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone lib="NICHD_XGC_Emb6"
lab_host="DH10B"
note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                     AUTHORS
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Klauener, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="COG2319; Region: FOG: WD40 repeat [General function prediction only]" | /db_xref="CDD:COG2319"
                                                                                                                                                                                                                                                                                          /db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /traislation="FFRQGKILVGTRNSEIIEVGEKNAACNILVNGHVDGPIMGLATH
PSRDFPLSAAEDGTVRLWDIADKKMINKVNLGHAARTVCYSPEGDMVAIGMKNGEFII
LLVSSLKINGKKRDRRCAIHDIRFSPDSRYLAVGSSBNSVDFYDLTGFFILNRISYCK
BYDT ISFVIQMPSADSRHLQVSGCTKRHVYEVPSGKHLVDHAAIDRITWATWTSILGD
BVMGTWSRHAEXAADVCACVSHSGISLVTGDPFGMVKLYDFPCPEKFFAKHKRFLGHSP
HVTNIRFTSGDRHVVSAGGDDCSLFVWKCVHMPH"
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                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plates 6 Row: o.Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 04-NOV-2003
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2266)
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Homo sapiens KIAA1277 protein, mRNA (cDNA clone IMAGE:4445131),
partial cds.
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100.0%; Pred. No. 5.5e-13;
cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein id="AAH27154.1"
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| db xref="LocusID:217820"
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                                                                                                                                                                                                                                 'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="LOC217820
                                                                                                                                                                                 Location/Qualifiers
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/gene="LOC217820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="LOC217820"
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                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="FVB/N"
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A.N., Gibbs, R.A.
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BC049193
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ORIGIN

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CDS

FEATURES

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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergeren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.T., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
E 22382257

E 2238225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcompril.nih.gov/
Contact: nisc_mgcompril.nih.gov/
Ackhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Grannite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Peargoon, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Young, A., Zhang, L.-H. and Green, E.D.
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Location/Qualifiers
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REKKRKIPKTUTRINAIYEURRGKKKYKRLSQBRENBGKPEKLKA
HSQRLWNVKSRLKQBPRYEGLFBYRYRLSQBRSNGGKPEKLKA
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FYCRLLDGSKGKRLPRYGTUSRLGCFSLFSRLLDBYKRKAGTSPALVQPLMSWMEA
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LERRVIFIADKLSILGKCCHAMVALIYPFAMQHTYIPVLPPAMVDIVCSFTFFLIGLL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 2266)
Strausberg, R.
Direct Submisser, R.
Submitted (21-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue type="Liver, adenocarcinoma"
/clone lib="NIH MGC 90"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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2 (bases 1 to 2389)
Strausberg, R.
Direct Submission
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                   polyA_signal
polyA_site
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Matches
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AUTHORS
TITLE
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VERSION
KEYWORDS
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PUBMED
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COMMENT
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LOCUS
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Martinsried, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This close (DKEZp434C2016) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.bicohem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="dDENN, Region: dDENN domain. This region is always found associated with pfam02141. It is predicted to form a globular domain. This domain is predicted to be completely alpha helical. Although not statistically supported it has been suggested that this domain may be similar to members of the Rho/Rac/Cdc42 GEF family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LANBO1945 2270 bp mRNA linear PRI 18-FEB-2000 Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016). AL137281
                                                                                                                                                                                                                                                                               /note="DENN; Region: DENN (AEX-3) domain. DENN (after differentially expressed in neoplastic ve normal cells) is a domain which occurs in several proteins involved in Rabmediated processes or regulation of MAPK signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
SSSLPLLRELPLEEVLVVDLVNSRFIRQMDDEDSILPRKLQVALEHILEGRNELACEG
DEPELGGRHGPESSPLMEVVSEAFVRFFVEIVGHYSLFLTGGEREERTLGREAPRKAV
SSKSLRHFLEVFMETQMFRGPIQERELRRQDAKGLFEVRAGEYLETLPSGEHSGVNKF
LKGLGNKWKFLHKK
                                                                                         557. .847
//gene="KIAA1277"
//note="uDENN; Region: uDENN domain. This region is always
found associated with pfam02141. It is predicted to form
an all beta domain"
//db_xref="CDD:pfam03456"
866. .1330
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/map="433.4 cR from top of Chril linkage group"
/clone="DKFZp434C2016"
/tissue type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 2270)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
Direct Submission
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1.3%; Score 49; DB 9; Length 2266;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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1571. .1774
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                                                                                                                                                                                                                                                           /gene="KIAA1277"
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 77
HSM801945
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AUTHORS
TITLE
JOURNAL
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 2389)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.K., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonddo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Human and mouse onwa semience
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROD 12-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: agapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 2270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC064017 2389 bp mRNA linear Mus musculus cDNA clone IMAGE:3995710, partial cds.
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                Local Similarity 100.0%; Pred. No. 5.5e-13; les 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                              DB 9;
DH10B, sites NotI + Sall"
/dev stage="adult"
2189. .2194
2207
                                                                                                                                                                                                                                         Score 49;
Pred. No.
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Mus musculus
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BC064017.1 GI:39794122
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source
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ACCESSION
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BC053126
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REMARK
COMMENT
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In (bases 1 to 2507)

Strauberg, M.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausherg, R.L., Zeeberg, B., Butch, K.H., Schamen, C.M., Schuler, G.D.,

Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Maruslina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleron, M., Soares, M.B., Bordando, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Smallus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and mouse chan listial analysis of more than 15,000 full-length
                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 131 Row: g Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27370269. Location/Qualifiers
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Mus musculus solute carrier family 43, member 1, mRNA (cDNA clone MGC:59491 IMAGE:6330614), complete cds.
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                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI CGAP_Lu29" /lone_lib="NCI CGAP_Lu29" /lab host="NH10B" /lab host="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.3%; Score 49; DB Best Local Similarity 100.0%; Pred. No. 5.5 Matches 49; Conservative 0; Mismatches
                                                                                                                                                                                        1. .2389
/organism="Mus musculus"
/mol type="mRNA"
/strain="czech II"
/db.xref="taxon:10090"
/clone="IMAGE:3995710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sednences
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PUBMED
REPERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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BC053747
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KEYWORDS
SOURCE
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                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRIGIN
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셤 8

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cDNA Library Preparation: Reeden, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bogsc.bc.ca info@bogsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Galland, Ran Guin, Eletticia Hisiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Vang, Scott Zuyderduyn, Marco Marra.
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PRPIRIUGSACFAASCTLMALASRDTBYLSFLIFLALSLNGFAGICLTFTSLTURNMF
GNLRSTFRMALMIGSYASSATTPPGIKLIYDAGVPFTVIMFTWSGLACLIFLENCALNNP
ARAFPAPEBUDYTKKILLIGLALDHKVTGDRFYTHVTIVGQRLSQXSFSBLEEGADAFI
SSPDIPGTSEETPEKSVPFRKSLCSPIFLWSLVTWGNTQLRVIFYMGAMNKILEFIVT
GGKREETNGRQKQKTSETVRFYSSIFGYMQLLCLLTCPLIGYINDRRIRGCYDDAFTEGT
INBNASFGDARGGASTWFTRPRYRVQXLTNALLIVGFGIACLIKNLHLQ
ILLAFVLHIYVRGPFRASACGGLYAAVPPSNHFGTLTGLIGSLISAVFALLQQLLIKNLHLQ
PLHGDPFWVNLGLLLLSFLGFLLPSYLYYRSRLQREYATNLUVDFQKVINTSKVAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 109 Row: b Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Embryo, day 9 mouse (C57BL/6 background)
otocysts"
/close 11b="NIH MGC_130"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC053126 2582 bp mRNA linear VRT 08-OC'
Danio rerio cDNA clone MGC:63875 IMAGE:6789528, complete cds.
BC053126
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100.0%; Pred. No. 5.5e-13;
cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MGC:59491 IMAGE:6330614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonyms: PB39, R00504"
(db xref="LocusID:72401"
(db xref="MGI:1931352"
(db xref="MGI:1931352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="Slc43al protein"
protein id="AAH53747.1"
(db_xref="GI:31753064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .2507
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="Slc43a1"
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Best Local Similarity 100.0
Matches 49; Conservative
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PAT 12-AUG-2002
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  ndmitrrslgyayvnfoopadaeraldimnfdvvkgkpirimmsordpslrksgvgn
                                                                                                                                                                                                                                                                                     429. .1301
/note="COG0724; Region: RNA-binding proteins (RRM domain)
[General function prediction only]"
/db xref="CDD:COG0724"
1809. .2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/note="PABP; Region: Poly-adenylate binding protein,
unique domain"
/db_xref="CDD:pfam00658"
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Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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Cd2000 and cd2001 molecules and uses thereof
Cd2000 and cd2001 molecules and uses thereof
Patent: BP 1223218-A 1 17-JUL-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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1.3%; Score 49; DB 6; Lo
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0;
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Sequence 31 from Patent EP1223218.
AX474270 GI:22213882
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Sequence 1 from Patent EP1223218.
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

(Ypriniformes; Cyprinidae; Danio.

I (Dases 1 to 2582)

I (Callas, F.S., Wagner, L.H., Derge, J.G., Klausner, R.D., Shemmen, C.M., Schuler, G.D., Altschul, S.F.; Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatcherko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brange, C., Raha, S.A., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalan, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, R., Young, A.C., Shevbenko, Y., Bouffard, G.G., Blakesley, R.W., Young, A.C., Schwutz, J., Myers, R.M., Schein, J.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J. Procontrol of the sequences on the sequences of the se
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

1. .2582
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Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site:

Contact: (Dickson, Mark) med@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg, R.

Direct Submission
Submitted (02-JUN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iuman and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12388257
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BC053126.1 GI:31419251
                                                               Danio rerio (zebrafish)
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PAT 12-AUG-2002

REFERENCE AUTHORS TITLE JOURNAL

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Dukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12 (bases 1 to 2789)
Straubberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garda, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madal, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens solute carrier family 22 (organic anion/cation
transporter), member 12, transcript variant 1, mRNA (cDNA clone
MCC:61679 IMAGE:5183650), complete cds.
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1.3%; Score 49; DB 6; L.
1. Similarity 100.0%; Pred. No. 5.4e-13;
49; Conservative 0; Mismatches 0;
                                                          Query Match
1.3%; Score 49; DB 6; L4
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Seguence 34 from Patent EP1223218.
AX474273 GI:22213885
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Cd2000 and cd2001 molecules and uses thereof
Parent: EP 1223218-A 32 17-JUL-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                            Praser, C.C. cd2001 molecules and uses thereof cd2000 and cd2001 molecules and uses thereof Patent: EP 122318-A 31 17-JUL-2002; Millennium Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 5.4e-13;
:ive 0; Mismatches 0;
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1.3%; Score 49; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0;
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Sequence 33 from Patent EP1223218.
AX474272
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Sequence 32 from Patent EP1223218.
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Matches 49; Conserva
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 83 AX474271 LOCUS 83

REFERENCE AUTHORS TITLE JOURNAL

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DGILLCKMINFSQPDTIDERAINKKKLTPFFISENNALANSASAIGCTVVNIGSQDL
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NYHLANAGWQKISNFSQDIRDSRAYYHLLNQIAPKGDDFDBEHVVELDPSGFNDKNDLR
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LSDLGBGEKKNDEIIIKWNNQTLANNKKYSITSFKDKSISTELPVLIDALIARRAYTLNV
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 2803) de Arrida, M. V. Watsudaira, P. de Arrida, M. V. Watsuda, S. Lin, C. S., Leavitt, J. and Matsudaira, P. Pimbrin is a homologue of the cycoplasmic phosphoprotein plastin and has domains homologues with calmodulin and actin gelation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (15-MAR-1990) Arruda de M.V., Whitehead Institute for
Biomedical Research, Nine Cambridge Centre, Cambridge MA 02142,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_trpe="mRNA" | Selection | John State | 
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100.0%; Pred. No. 5.4e-13;
tive 0; Mismatches 0; Indels
                                                                                                               Length 2789;
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                                                                                                                                                  5.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                           1.3%; Score 49; DB 9;
llarity 100.0%; Pred. No. 5.4e-1.
Conservative 0; Mismatches
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J. Cell Biol. 111 (3), 1069-1079 (1990)
90361735
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/db_xref="CDD:pfam00083"
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X52562
X52562.1 GI:62889
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Gallus gallus
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Arruda de, M.V.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Rhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Gudn,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Tquchman,J.W.,
Teurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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WWLAESARWLLTTGKLDWGLQBLWRVAAINGKGAVQDTLTPEVLLGARREELSWGQPP
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KWGALLLLSHLGREFTLAASLLLAGLCI LAWTLVPHEMGALESALAVLGLGVGAAFT
CITIYSSELFPTVLRWTAVGLGQMAARGGAILGPLVRLLGVHGPWLPLLVYGTVPVLS
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pshrcwapilidnstagasilgsispeallaisippeppnorphycrreqoqwolliden
atatswseadtepcydgwydrsiftstivakmnivodshalkpmagsiylagilyga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 115 Row: c Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24497484.
Location/Qualifiers
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/lab host="DH10B"
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywineki, M.I., Skaleka, U., Sanalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
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738. .1859
/note="sugar_tr; Region: Sugar (and other) transporter"
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-UNN-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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| gene="SLC22Al2"
| forte="synonyms: OAT41, URAT1, RST"
| db xref="LocusID:116085"
| db_xref="MIM:607096"
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/trānslation="meerrphidarprnshtnhropvdgelpprarnoannppanali
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clone="IMAGE:4546448"
                                                                                                                                                                                                               note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                             gene="KIAA1404"
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gene="KIAA1404"
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On Aug 19, 2003 this sequence version replaced gi:15559352.
On Aug 19, 2003 this sequence version replaced gi:15559352.
Ontact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgcahpgi.nih.gov/
Contact: nisc.mgcahpgi.nih.gov/
Nchter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Lagaspi.R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Passon,C., Vogt,J.L., Waltker,M.A., Wetherby,K.D., Wiggins,L.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M. B., Bonddo, M.F., Casarant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrameon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.U.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, C., Helten, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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Location/Qualifiers
                                                                                                                                                                 BC014041 2810 bp mRNA linear PRI 05-NOV-2003
Homo sapiens XIAA1404 protein, mRNA (cDNA clone IMAGE:4546448),
partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2810)
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Submitted (10-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
BC014041.2 GI:33874124
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                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
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BC014041
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TENTRICATE ACTUAL TATALETA INTEREST CATALOGUE LENGUAGE CONTROLLE C
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Weber, E.R. and McCall, C.A.
Weber, E.R. and McCall, C.A.
Canine low affinity IgE receptor (CD23) nucleic acid molecules and
uses thereof
Patent: US 6410714-A 1 25-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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1.3%; Score 49; DB 6; Length 2851;
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
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1.3%; Score 49; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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FEATURES

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HCU29643 3049 bp mRNA linear ROD 11-DEC-2003
Mus musculus RIKEN CDNA 2810408E11 gene, mRNA (CDNA Clone MGC:25768
HMAGE:4010810), Complete cds.
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EREDDEEBEDEDBI KKELDEPHSPCTAVASSSSDYPQSSTUVTAEVKDEOGRESSTO
SEVVENGVURSTSEDDS PDSSHAATGSESDPKEQQABEEEBERSAEAQSTEETNDPVSS
SSNNSSDEGVSSAETPSSASPSSSTELPAEGSVTARITSDNSETADDNMEQD
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TSEKKGSSCVNRANGYMFPGNTSAFPDRNVNGPGTPRPLARFRGSSWARTWGLPDS
                                                                                                                                                                                                                                              Washington

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

B. M. Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan E. Brockerhoff, University of Washington
cDNA Library Preparation: Susan E. Brockerhoff, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7955"
/clone="IMAGE:4144592"
/tissue_type="Eye, adult retina, 1-2 year old, mixed sex"
/clone_lib="cebrafish adult retina cDNA"
/lab_host="DH108"
Direct Submission
Submitted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 136 Row: b Column: 8.
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Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript SK-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
Mus musculus
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BC029643.1 GI:20987279
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

I Chases 1 to 2054)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Alaschul,S.F., Gollins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Gordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninoi,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullay,S.J., Bosak,S.A., McEwan,P.J.,
Norley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Fahey,J., Helle,S., Garcia,A.M., Madan,A., Rodrigues,S.,
Sanchez,A., Whilling,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalaka,U., Snallus,D.E.,
Schnerch,A., Schein,J.E., Onses,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
VISBBERGE
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                                                                                                                                                                               PAT 25-SEP-2002
                                                                                                                                                                                                                                                                                                                                                       Unclassified.

1 (bases 1 to 2851)

1 (bases 1 to 2851)

2 (bases 2 to 2851)

Canine low affinity IgE receptor (CD23) nucleic acid molecules and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.3%; Score 49; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: US 6410714-A 3 25-JUN-2002;
Location/Qualifiers
1.,2851
                                                                                                                                                                             AR216298 2851 bp
Sequence 3 from patent US 6410714.
AR216298.1 GI:23314768
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2 (bases 1 to 2954)
Strausberg,R.
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AR216298/c
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SALLDFLSSYERGYLGYFERSGROPPGYLFFTSALHSLKKDYLGTVRFGVITDKHL
SALLDFLSSYERGYLGYFERSGROPPGYLFFTSALHSLKKDYLGTVRFGVITDKHL
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LLLANNELKKGPALFLFIP PPPDLAREHPLLDEI TEVALEYNNCHGDQVVERLLGHLGRV
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SRGNAS FTGSEQNYLTREYTKEGTFYHVVGSEIESCNFLTSYSPEGVGTACRTI
SRGNAS FTGSEQNYLTREYTHGOFTSACPTGAPTAGTTU
MKFTLESFLQNFSYTYSPLKGHTTGSBASQFPTGHLLTTGYTTOFTTOFTOFTGAT
YTTQNCGFCPSLNHIFIOLARLLFSDSACPTGATTTTOTTOFTFWETWTLKGDVLLL
YTTQNCGFCPSLNHIFIOLARLLFSDSTFTVARIDVGNGTRWFTLKROVLLLEFPCN
YTTQNCGFCPSLNHIFIOLARLLFSDSTFTVARIDVGNGTRWFTLKROVLLEFPCN
HVBRNANGKLSBERSSLRRTQGQVGGRILLSRANGHLLRRHSQKL
QALYLKKARBLQELARAGFPLPBHTWLKILLYNTWERELBGQGGAKBPAPLGKARPNH
SKEMGTTQLPGDTFPPSTTSSTLASSTKHBRNTD"
                                                                                                                                                                                                                                                                                                                                                                                                                          small enzymes that participate in redox reactions, via the reversible oxidation of an active centre disulfide bond. Some members with only the active site are not separated from the noise"
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2 (bases I to 3072)

2 (bases I to 3072)

Direct Submission

1 - Chome, Shinjuku-ku, Tokyo 162-8640, Japan

1 - Chome, Shinjuku-ku, Tokyo 162-8640, Japan

(E-mail:khabhi@nli go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111 (ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        small enzymes that participate in redox reactions, via the reversible oxidation of an active centre disulfide bond. Some members with only the active site are not separated
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Macaca fascicularis brain cDNA clone:QtrA-14469, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xref="CDD:pfam00085"
2007. .2327
/note="thiored; Region: Thioredoxin. Thioredoxins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleo
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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0
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100.0%; Pred. No. 5.4e-13;
iive 0; Mismatches 0;
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="CDD:pfam00085"
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AB063100.1 GI:14388574
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Best Local Similarity 100.0
Matches 49; Conservative
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ORGANISM
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AUTHORS
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AB063100
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Blatchenko, L., Maruelna, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Farange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergen, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, M., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Undnes, S.J., and Marra, M.A.
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RRGLRGASLMARQRPELLCGAVALGCALLFALKFTCSRAKDVIIPAKPPVSFFSSRSP
VLDLFGGQLDYADHVRQDSEVVVLFFYAPWCGGSIAARAEIEQAASRLSDQVLFVAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/ILML at: http://image.llnl.gov Series: IRAK plate: 30 Row: i Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:10090" /clone="MGC:25768 IMAGE:4010810" /clone="MGC:25768 IMAGE:4010810" /tissue type="Mammary tumor metastatized to lung. MMTV-LTE/Wnt1 model. Expression driven by an MMTV-LTR emhancer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk,
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.R. CORBOTTIUM (LINL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
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/product="expressed sequence A1427833"
/protein id="AAH29643.1"
/db xref="G1:0997280"
/"....f "#_....rn.116.000"
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/lab_host="DH10B"
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/db_xref="MGI:1923620"
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    .3049
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="Czech II"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 3049)
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Direct Submission
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Generation and initial analysis of more than 15,000 full-length
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Strausberg, R.
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Rlausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausher, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.M. B., Bonaldo, M.F., Casarant, T.L.,
Scheez, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallahy, S.J., Bosak, S.A., McEwant, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct DraIII sites of pWR185-Ff13. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of
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SPWPTLSISTLYLLFVWLGPKMKDREPFQMRLVLIIYNFGMVLLNFFIFRELFMGSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHCTWFTLWMIGIKWVAGGQAFFGAQMNSFIHVIMYSYYGLAAFGPWIQKYLWKRYL
TWLQLVQFHVTIGHTALSLYTDCPFPKWMHWALIAYAISFIFLFLNFYIRTYKBPKKP
KTGKTAMNGISANGVSKSEKQLVIENGKKQKNGKAKGD"
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 3124)
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Danio rerio cDNA clone MGC:63655 IMAGE:5612000, complete cds.
BC054927
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                   organism="Macaca fascicularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="hypothetical protein"
protein id="BAB60806.1"
db_xref="G1:14388575"
                                                                                                                                                                                                    Custom primer used for sequencing ( 5' end primer [CTGACTTAAAAGCTGCB]; 3' end primer [CGACTGCAGCTGAGCACAR]).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3C054927.1 GI:32766369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 94
BC054927
LOCUS
DEFINITION
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ORGANISM
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VERSION
KEYWORDS
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COLLECT: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
Tissue Procurement: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lissa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Nacasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 118 Row: o Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGIEQEGYMLPGDEMEQMSEGSKPSLPSEALFPDDWEAESHDWYCFECHLPGDVMECD
GCFRVYHLRCVSEDHRPRDTTSHWQCGICRGSKRKNINKQEMTTYLKFILGFWKERAV
DLHKSFEEFRADAQLIVHNTAILHGVNSDQTEIARLLYNDTCLLASCGPVFCARSPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MDRISRYLSRVYGMHPKDTARQLVLAVKDGLVVBTLTVGCKGSK
                                                                                                                                                                                                                 Direct Submission
Submitted (08-UUL-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
produc="unknown (protein for MGC:63655)"
protein id="AAH54927.1"
db_xref="GI:32766370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483. 617
/note="PHD; Region: PHD zinc finger"
/db_xref="CDD:smart00249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Danio rerio"
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/mol_type=maxNa"
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/clone="MGC:63655 IMAGE:5612000"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627. .818
/note="BROMO; Region: bromo domain"
/db_xref="CDD:smart00297"
                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
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100.0%; Pred. No. 5.3e-1:
ive. 0; Mismatches
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 95 BC036825

REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

The (bases 1 to 3114)

R Nambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission

AL Shameted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152

Martineried (10-MAR-1999) MIPS, Am klopferspitz 18a, D-82152

This clone (DKFR5) Email aviental Am klopferspitz 18a, D-82152

This clone (DKFR5) MIPS, DRAMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.blochem.mgg.de/proj/cDNA/.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Es Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstean, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3290 bp mRNA linear ROD 16-APR-2003
Mus musculus RIKEN CDNA 9530006B08 gene, mRNA (cDNA clone
IMAGE:5322259), partial cds.
                                                    HSMB00211 3174 bp mRNA linear PRI 18-FEB-2000
Homo sapiens mRNA; cDNA DKFZp586C241 (from clone DKFZp586C241).
AL049426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="uterus"
/clone_lib="586 (synonym: hute1). Vector pSport1; host
DH10B; mitem NotI + SalI/MluI"
/dev_stage="adult"
3118. 3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3174;
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100.0%; Pred. No. 5.3e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/db_xref="R2DD:DKFZpS86C241"
/clore="DKFZpS86C241"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC032176.1 GI:21595134
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Best Local Similarity 100.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                  Homo sapiens
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polyA_site
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KEYWORDS
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DEFINITION
ACCESSION
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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BC032176
                 RESULT 96
HSM800211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Sile: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeelbey,R.W., Boufstad,G.G., Breen,K., Brinkley,C.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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PRRPIRPLETISTLAMLVTSDMYTLINYVGFINYLFYGGYTVAGQIVLRWKKEDDI
PRPIKPLPYQG"
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                     PRI 26-AUG-2002
                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3145)
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                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (13-MUG-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="IMAGE:5191998"
/tissue_type="Brain, adult, 6 pooled whole brains"
/clone lib="NHH MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Homo sapiens, clone IMAGE:5191998, mRNA, partial cds.
EÇ036825
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                                                                                                                BC036825.1 GI:22477362
                                                                                                                                                                                   sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                        Strausberg, R.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0ery Match
Best Local Similarity 100.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analysis.
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BC034128
LOCUS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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COMMENT
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcambgrl.nih.gov/
Contact: nisc_mgcambgrl.nih.gov/
Contact: nisc_mgcambgrl.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Guten,Y., Haghighi,P.,
Mansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Peargen,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plates 56 Row: 1 Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Worlladon, D.K., Muzny, D.M., Sodergran, E.J., Lu, X., Gibbs, R.A.,
Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeelley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Beneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (06-UNN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAH32176.1"
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Strausberg, R.
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NH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Conter, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRRX plate: 44 Row: 1 Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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NUQKAVRAKSVMGRQTCLECSFETEPPRHFPTVTVHGGLCRSTGCSRATAAHIN
NHVPRKS PKYLALFROSVSGIKLACTSCTEPETPPPRHFPTVTVHGGLCRSTGOSRATAAHIN
NHVPRKS PKYLALFROSVSGIKLACTSCTPATSVGDAMAKHLJFPRGE
SWASHLIR PGQASER VPDWSMRNTYLPP PLVPNKAATVKPVGVTPABPGPLAGPULQAL
PSPASTATPPATPTHPQPSALPPATEGTECLAVSRQEBEGSPTVQDPBPASGGGGGS
VGKKGQLSVKKLRVVLRALCCNTEQDAEHFRUPQRRITRRMLRRFQASGGGGSG
VGKKGQLSVKKLRVVLRFQABAEHFRUPQRRITRRMLRRFQASGGGUSGKYLS
PRAERIAEWYLI OFFECTIVPROPAEHFRUPQRSTRIRMLRRFQASGGGULGGKYLS
PRAERIAEWYLI OFFECTIVPROPAEHFRUPQRSTRIRMLRRFQASGGRILGGKYLS
PHARRAVAHTLPKHVAENAGLFIEFVQRQIHNQDLPLSMIVAIDELELFLDTEVLHSD
                                                                                                                                                                                                                                                                                                                                  DRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFFRGQANRPANVPDS1LLEAKDSG
YSDDEIMELMSTRVMKKHTACCHSKBALVMDCHFTHISBEVLALLSASSTLPANVPAG
CSSKIOPLDVCIKRTVMRTHLKKWKRARAARDAACDSDVLLQLVLWHGEVLGVUGD
SPELVQRSELVANVELGEDGRVNSPTRNADMCEELIASLEBQLKLMGEQSEEHSASAP
RPRSSPEETVEPESLHQLFEGESETESPYGFERADLDLMEI"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 3387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="raxon:10090"
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/tissue type="Salivary gland, 10 week old female mouse"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3387 bp mRNA linear ROD 20-SEP-2
Mus musculus, Similar to neuronal specific transcription factor
DATI, clone IMAGE:4913908, mRNA, partial cds.
BC034128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 5.3e-13;
tive 0; Mismatches 0; Indels
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DRIGIN

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Gaithersburg, Maryland;
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Malak, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Malak, M., Soderia, A.M., Gay, L.J., Hulyk, S.W.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Kazywinski, M.I., Schalu, J., Whers, R.M.,
Butterfield, Y.S., Kazywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and mouse oDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3563 bp mRNA linear PRI 03-OCT-2003
Homo sapiens syndecan 3 (N-syndecan), mRNA (cDNA clone MGC:12759
RGN19074
RGN19074
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MKEGYAPQVR"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3563)
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Submitted (10-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                              Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:15559238.
Contact: MGC help desk
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0
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100.0%; Pred. No. 5.3e-13;
tive 0; Mismatches 0; Indels
  note="Vector: pCMV-SPORT6"
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                                                                                                       factor DAT1"
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                           .341
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Best Local Similarity
Matches 49; Conserva
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KEYWORDS
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AUTHORS
TITLE
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BC013974
LOCUS
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TITLE

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tpppetfititrdpepevygggscoppelpsetyopotaansvvavggaaakassppg
tlpkgarpgpellunaldsgssaaqlpoksilerkevluavivggvvgalfaaflut
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                  found
                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 17 Row: f Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7662137.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Syndecan; Region: Syndecan domain. Syndecans are
transmembrane heparin sulfate proteoglycans which are
implicated in the binding of extracellular matrix
components and growth factors"
/db_xref="CDD:pfam01034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _note="synonyms: KIAA0468, SDCN, SYND3"

db_xref="LocusID:9672"

db_xref="MIM:186357"

cb_xref="MIM:186357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIYRMKKKDEGSYTLEEPKQASVTYQKPDKQEEFYA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.3%; Score 49; DB 9; L.
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAH13974.1"
db_xref="GI:15559239"
db_xref="LocusID:9672"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="SDC3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC028880.1 GI:20810021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .. .3563
'gene="SDC3"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, B.
Altechol, S. F., Zeeberg, B., Bueterow, K.H., Schaefer, C.F., Bhat, N.K.,
Hoppins, R.F., Jordan, H., Moore, T., Wang, J., Halph, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriques, S.,
Sanchez, A., Whiting, M., Madan, A., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Kzzywinski, M. I., Skalska, U., Schmutz, J.,
Butterfield, Y.S., Kzzywinski, M. I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:4163231"
/clssue_type="Liver, normal. 5 month old male mouse."
/clone_lin="NGI CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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AUTHORS
TITLE
JOURNAL
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MEDLINE
PUBMED
                                      REFERENCE
AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
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Gaps

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1.3%; Score 49; DB 10; Length 3608; 100.0%; Pred. No. 5.3e-13; tive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 49; Conservative ନ ନ

Search completed: April 23, 2004, 08:22:46 Job time : 14172 secs

Sequence 1 Sequence 1 Sequence 1 Sequence 1	Sequence 5 Sequence 6 Sequence 1 Sequence 7 Sequence 7	Sequence 7 Sequence 7 Sequence 7 Sequence 9	Sequence 7	Sequence 4 Sequence 2 Sequence 7	Sequence 1 Sequence 7	Sequence 2	Sequence 1 Sequence 1	Sequence 1	Sequence 1 Sequence 1	Sequence 3 Sequence 9 Sequence 1	Sequence 1	Sequence 1 Sequence 1 Sequence 1	Sequence 1 Sequence 1	Sequence 1	Sequence 2	Sequence 2	Sequence	Sequence 1	Sequence 2	Sequence 4	Sequence	Sequence 4	Sequence 2	Sequence	Sequence 1	Sequence	Sequence 2	Sequence		
sn sn sn sn	4 US-09-105-542A-2 4 US-09-381-488-6 1 US-08-665-716-1 2 US-08-713-000-7 2 US-08-975-316-7	SSSSS	s s s	SS SE	SSS	SSS	SD	888	SS	8888	S S	SD	SD	Sus	US US	us us	323	US US	SS SS	SU	SS	252	SD	SS	SD	go	SD	SD	820-004- 522-714-	
352 362 371	615 975 1147 1454	1454 1454 1454 1460	1460 1474 1474	1474	1474	10288 13414	189	1199	199	233 233 242 242	242 246	22 22 24 44 29 20 20 20 20 20 20 20 20 20 20 20 20 20	5 5 7 8 5 8 8 5 8 7 8	7 0 0 0 0 0 0 0 0 0 0 0	700	890	9 6	953 997	1032	1071	1138	1153	1192	1279	1315	1477	1503	1503	1606	
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28 29 31 33 31	1 W W W W C	2 t w w w 4 .	4 4 4 4 4 4 4	4 4 4 4	0444°	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		# KA (VA)		61	166	666	80 O C	77772	C 73	75	77	908	81	. 833	# VO :	86	88 0	000	76		#:	0.60	100	
Ltd.	time 244 Seconds	ion cell updates	aaaaaaaaaaaa 3762			1365418			*. *	* * * * \$ 9	: * :: ::	<pre>l by chance to have a the result being printed, re distribution.</pre>		Description	=	01 (1)		a, n,			v ==	~~		Sequence 10051, A Sequence 10050, A				, ,,	Sequence 16028, A Sequence 16058, A Sequence 16008, A	
GenCore version 5.1.6 (c) 1993 - 2004 Compugen	ing sw model 03:54:40 ; Search	8556.2	cactgtgaaaaaaaaa	•	277475446 residues	g chosen parameters:	000	150 summaries	.odata/2/ina/5A_COMB.seq	/cgn2_6/ptodata/2/ina/5b_COMB.seq:* /cgn2_6/ptodata/2/ina/6b_COMB.seq:* /cgn2_6/ptodata/2/ina/6b_COMB.seq:*	odata/2/ina/backfīles1.	esults predicted to the score of the total score	SUMMARIES	OI EO		US-08-909-969					US-U9-201-6/4-2 US-09-621-976-19	US-09-621-976-16 US-09-621-976-16	US-09-621-976-16	US-09-621-976-16	US-09-621-976-16 US-09-621-976-16	US-09-621-976-16	US-09-621-976-16	US-09-621-976-16	4 US-09-621-976-16026 4 US-09-621-976-16058 4 US-09-621-976-16008	
Gopyright (c	nucleic search, us April 23, 2004,	us 37	1 gagaaaccgag	Gapop_60.0 ,	682709 seqs, 2 0	of hits satisfying	q length: 0 q length: 200000000	ng: Listing first	1881	2: /cgn2_6/pt 3: /cgn2_6/pt 4: /cgn2_6/pt		No. is the number of r greater than or equal s derived by analysis o		* Query Match Length	9 1.3 159		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1.3	11.3	12.	7 1.2	7.1.2	14,	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.2	4.5	444	1.2	47 1.2 347 47 1.2 357 47 1.2 359	
	nucleic - 1	score	Sequence: Scoring table		Searched: Word size :	number	DB sed DB sed	Post-processing				Pred. N score g and is		Score	4	4.4	4.4	44	4.4	4.4	1.4	4.4	4' '	* 4r ,	4· 4	~ 4	. ~ ~	. 40	- 4· 4·	

Gaps

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Query Match 1.3%; Score 49; DB 2; Length 882; Best Local Similarity 100.0%; Pred. No. 2.8e-10; Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                       Query Match
1.3%; Score 49; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/0890965C
| Sequence 9, Application US/0890965C
| Sequence 9, Application US/0890965C
| Patent No. 5936078
| GENERAL INFORMATION:
| APPLICANT: Raya Tetero
| APPLICANT: Sakaki yochiyuki
| APPLICANT: Manhalda Hideji
| TITLE OF INVENTION: AND NOVEL DNINEDDY
| UNMERS OF SEQUENCES: 17 Perk Avenue
| CITY: New York | CITY: New York | CONTRINESSEE: 17 Perk Avenue
| CITY: New York | CITY: New York | CONTRINESSEE: PITZPATRICK CELLA, HARPER AND SCINTO
| STREET: New York | CONTRINESSEE: PITZPATRICK CELLA, HARPER AND SCINTO
| STREET: New York | CONTRINESSEE: PITZPATRICK | CITY | CITY | PITZPATRICK | CITY | CITY | CITY | PITZPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 97 to 195
IDENTIFICATION METHOD: by experiment
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          JS-09-621-976-17182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-08-909-965C-9
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Sequence 1, Al
Sequence 1, Al
Sequence 1, Al
Sequence 48, A
Sequence 48, A
Sequence 4, Ap
Sequence 19, Sequence 119, Sequence 113, Sequence 31, Sequence 31, Sequence 31, Sequence 16, Seq
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Sequence
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Sequence 17182, Application US/09621976

Sequence 17182, Application US/09621976

Patent No. 6639063

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobcart, S.,

APPLICANT: Joicdano, J.Y.

TILLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 17182

LENGTH: 159

TWOMER OF SECTION NUMBER: DEST OF SECTION NUMBER 
                                                                                            US-09-000-066-1

US-08-045-144A-1

US-08-060-0213

US-08-060-0213

US-08-060-0213

US-08-074-691-7

US-08-074-691-7

US-09-074-691-7

US-09-076-166-16

US-09-09-195-666A-16

US-09-09-195-666A-16

US-09-09-195-666A-16

US-09-019-618-10

US-09-019-10-10-10

US-09-01-11-10-11

US-09-07-17-10-11

US-09-07-794A-48

US-09-07-794A-48

US-09-07-794A-48

US-09-07-794A-48

US-09-01-794A-48

US-09-01-794A-48

US-09-01-794A-48

US-09-01-794A-48
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US-10-072-094-94
US-10-164-595-9
US-10-164-595-5
US-08-599-455B-3
US-09-069-781B-3
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Gaps

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-621-976-9448
                                                                                                                                                                                                                              SEQ ID NO 3
LENGTH: 2851
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APPLICANT: Weber, Eric R.

TILLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

TILLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/535,521

CURRENT FILLING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/125,913

EARLIER PRILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE PATENTY OF 2.1

ERROTH: 2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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1.3%; Score 49; DB 4; Length 1933;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 49; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Brenda F. Baker
TITLE OF INVENTION: ANTISENSE MODULATION OF SAP-1 EXPRESSION
FILLE REPERENCE: RTS-0267
CURRENT APPLICATION NUMBER: US/09/920,759
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 91
LENGTH: 1933
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1.3%; Score 49; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 49; Conservative 0; Mismatches 0;
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US-09-535-521-3/c
; Sequence 3, Application US/09535521
; Patent No. 6410714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09535521
Patent No. 6410714
GENERAL INFORMATION:
                                                                                            RESULT 3
US-00-920-759-3
; Sequence 3, Application US/09920759
; Patent No. 6537811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (150)...(1445)
US-09-920-759-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1077)
US-09-535-521-1
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: WCALL, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CANINE LOW MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT PILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER APPLICATION NUMBER: 60/125,913
SARLIER PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTING VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 94401, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Glodert, S.
TITLE OF INVENTION:
CURRENT APPLICATION WINBER: US/09/621,976
CURRENT PAPPLICATION WINBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.3%; Score 49; DB 4; L
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 49; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-08-05
EARLIER PILING DATE: 1998-08-05
EARLIER PILING DATE: 1998-08-05
EARLIER PILING DATE: 1998-08-05
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Patent No. 6476195
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; Canis familiaris
CORGANISM: Canis familiaris
US-09-535-521-3
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; OTHER INFORMATION: Description of Artificial Sequence: Target analyte US-09-183-619-1
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APPLICANT: DELLINGER, DOUGLAS J.
APPLICANT: DAHM, SUBANN C.
APPLICANT: ILSLEY, DIANE D.
APPLICANT: ACH, ROBERT A.
APPLICANT: TROLL, MARK A.
TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
TITLE OF INVENTION: HYBRIDIZATION NAMER: US/09/183,619
CURRENT APPLICATION NUMBER: US/09/183,619
CURRENT FILING DATE: 1998-10-30
BARLIER FILING DATE: 1996-10-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2%; Score 47; DB 2; Length 105; Best Local Similarity 100.0%; Pred. No. 2.1e-09; Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.2%; Score 47; DB 3; Length 105; Best Local Similarity 100.0%; Pred. No. 2.1e-09; Matches 47; Conservative 0; Mismatches 0; Indels
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,381
FILING DATE: 21-0CT-1996
CLASSITCATION: 435
ATTORNEY/AGRIT INFORMATION:
NAME: Choi, Wendy A: 36,697
REGISTRATION NUMBER: 36,697
REGISTRATION NUMBER: 36,697
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERPAK: 650-857-4125
TELERPAK: 650-857-8063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09183619
Patent No. 6103474
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 348-461
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: PANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 105
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Sequence 14, Application US/09187999A

Batent No. 6482646

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: diadulis, Frank
APPLICANT: diadulis, Frank
TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
FILE REPERENCE: CL-1321
CURRENT APPLICATION NUMBER: US/09/187,999A

CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 39

SOFTWARE: Microsoft Office 97

FENDING 14

FENDING 14

FENDING 14
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100.0%; Pred. No. 6.5e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.3%; Score 48; DB 4; Length 619;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08735381

Sequence 2, Application US/08735381

Fatent No. 5853993

GENERAL INPORATION:

APPLICANT: Dahm, SueAnn

APPLICANT: Troll, Mark

TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hewlett-Peckard Company, Legal Dept.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Intellectual Property
1501 Page Mill Road, MS 4U-10
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER PILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SEQ ID NO 58
LENGTH: 619
                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
LOCATION: (526)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (619)
COTHER INFORMATION: n equals a,t,g, or US-09-489-847-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA; CRGANISM: Lycopersicon esculentum US-09-187-999-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-187-999-14
                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                           Length 165;
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                                                                                                                                                                                         Query Match
1.2%; Score 47; DB 4; Length 165
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16913, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
    APPLICANT: Dumas Milne Edwards, J.B.
    APPLICANT: Jobert, S.
    APPLICANT: Glordano, J.Y.
    TILE OF INVENTION: ESTS and Encoded Human Proteins.
    FILE REFERENCE: GENSET: 054PR2
    CURRENT APPLICATION NUMBER: US/09/621,976
    CURRENT FILING DAIE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
    SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.2%; Score 47; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 47; DB 4; I
100.0%; Pred. No. 1.9e-09;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 1624
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16024, Application US/09621976
Patent No. 6639063
                  NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 19195
LENGTH: 165
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Dest Local Similarity 100.0
Matches 47; Conservative
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; ORGANISM: Homo sapiens
US-09-621-976-16024
                                                                                                                          ; ORGANISM: Homo sapiens
US-09-621-976-19195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-621-976-16813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-621-976-16024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 16813
LENGTH: 266
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ZIP: 94304-1126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/201,674
FILING DATE: 30-No. 6110882-1998
CLASSIFICATION PATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
                                                                                                 Sequence 2, Application US/09201674
Patent No. 6110682
GENERAL INFORMATION: GENERAL INFORMATION: Dellinger, Douglas J.
Dahm, SueAnn
Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
Intellectual Property
STREET: 1501 Page Mill Road, MS 4U-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Patent No. 6639063
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: SSTE and Encoded Human Proteins.
FILE REFERENCE: GENSET. 0549R2
CURRENT APPLICATION NUMBER: US/09/621,976
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1.2%; Score 47; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 47; Conservative 0; Mismatches 0;
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REFERENCE/DOCKET NUMBER: 10950427-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/735,381
FILING DATE: 21-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STEANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
TELEPHONE: 650-857-4125
TELEFAX: 650-852-8063
                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-621-976-19195
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100.0%; Pred. No. 1.5
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  NUMBER OF SEQ ID NOS: 19335
                 ; SOFTWARE: Parent.pm
; SEQ ID NO 16050
; LENGTH: 332
; TYPE: DNA
; ORGANIEM: Homo sapiens
US-09-621-976-16050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-16032
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US-09-621-976-16053
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US-09-621-976-16053
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1.2%; Score 47; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INTENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16012
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16031, Application US/09621976

Patent No. 6639063

GENERAL No. 6639063

APPLICANT: Dunas Mine Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

MUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
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US-09-621-976-16050
US-09-621-976-16050

Sequence 16050, Application US/09621976

Patent No. 6639663

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REPERENCE: GENSET.054PR2.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21
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Pred. No. 1.9e-09;
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                                                       RESULT 15
US-09-621-976-16012
VS-09-equence 16012, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-16031
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US-09-621-976-16031
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LENGTH: 332
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    Length 332;
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US-09-621-976-16032
US-09-621-976-16032
Sequence 16032 Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Globert, S.
TILLE OF INVENTION:
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICANTION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16032
LENGTH: 333
                                                                                                                                                                                                            Sequence 16653, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Gordano, J.Y.
ITLE OF INVENTION: BSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ 1D NOS: 19335
SOFTWARE: Patent.pm
Query Match
1.2%; Score 47; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
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1.2%; Score 47; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
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US-09-621-976-16013
Sequence 16013, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glocation, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENGET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
LENGTH: 336
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) Sequence 16041, Application US/09621976
) Patent No. 6639063
) GENERAL INFORMATION:
) APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
) TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
) CURRENT PILIOR DATE: 2000-07-21
) NUMBER OF SEQ ID NOS: 19335
) SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                   1.2%; Score 47; DB 4; Le
100.0%; Pred. No. 1.9e-09;
tive 0; Mismatches 0;
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1.2%; Score 47; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
FILE REFERENCE: GENSET.054PR2
CURRENT PEDLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16061
LENGTH: 335
                                                                                                                                                                               NAME/KEY: misc_feature; I-CCATION: 194 OTHER INFORMATION: n=a, g, c or t US-09-621-976-16061
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 47; Conservative
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; ORGANISM: Homo sapiens
US-09-621-976-16013
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                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                               FEATURE:
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                                        Sequence 16044, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INFORMATION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NORSER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 16044

LENGTH: 334
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Patent No. 6539063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glocato, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
1.2%; Score 47; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
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1.2%; Score 47; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: n=a, g, c or t
US-09-621-976-16044
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: 334
                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-621-976-16045
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RESULT 22 US-09-621

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, ORGANISM: Homo sapiens
US-09-621-976-16019
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US-09-621-976-16008
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                                                                                                                                                                                                                                                                                                     SEQ ID NO 16008
LENGTH: 359
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1.2%; Score 47; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 347;
                                                                           Length 338;
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Patent No. 6639063
GENERAL INPORMATION:
APPLICANT: UNDORATION:
APPLICANT: Glochano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Obmas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOPTWARE: Patent.pm
SEQ ID NO 16026
LENGTH: 310 100 16026
                                                                           Query Match
1.2%; Score 47; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                Sequence 16026, Application US/09621976; Patent No. 6639063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

1 LOCATION: 347

CTHER INFORMATION: n=a, g, c or t

US-09-621-976-16026
; LOCATION: 135,197
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-16041
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US-09-621-976-16058
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US-09-621-976-16058
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LENGTH: 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16019, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Goldano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION MUNERR: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOUTWARE: Patent.pm
SEQ ID NO 16119
LENGTH: 359
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; Sequence 16010, Application US/09621976
; Patent No. 6639063
; Patent No. 6639063
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Obert, S.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTE and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
Sequence 16008, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: GENGTANO, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; her-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Match 1.2%; Score 47; DB Local Similarity 100.0%; Pred. No. 1.9 les 47; Conservative 0; Mismatches
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JS-09-105-542A-2
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US-09-381-488-6
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                                                                                                                               Length 362;
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                                                                                                                                                                        Indels
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESYS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION UNBER: US/09/621,976.
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16048
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCORNATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOPTWARE: Patent.pm
SEQ ID NO 16642
LENGTH: 365
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1.2%; Score 47; DB 4; Li
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 47; Conservative 0; Mismatches 0;
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                                                                                                                               Query Match 1.2%; Score 47; DB 4; Lu Best Local Similarity 100.0%; Pred. No. 1.9e-09; Matches 47; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                          Sequence 16042, Application US/09621976 Patent No. 6639063
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Best Local Similarity 100.0%;
Matches 47; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-09-621-976-16048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16042
                                                                        ORGANISM: Homo sapiens
US-09-621-976-16010
SOFTWARE: Patent.pm
SEQ ID NO 16010
LENGTH: 362
                                                                                                                                                                                                                                                                                                                         JS-09-621-976-16042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-621-976-16048
                                                          TYPE: DNA
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Sequence 2, Application US/09105542A

Patent No. 6323329

GENERAL INFORMATION:

APPLICANT: Bullerdiek, Jorn

TITLE OF INVENTION: HIGH MOBILITY GROUP PROTEINS AND USES THEREFORE

TITLE OF INVENTION: HIGH MOBILITY GROUP PROTEINS AND USES THEREFORE

TILE REFERENCE: BOEHM4.001015.542A

CURRENT APPLICATION NUMBER: US/09/105,542A

CURRENT APPLICATION NUMBER: PCT/DE96/02494

PRIOR APPLICATION NUMBER: PCT/DE96/02494

PRIOR FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 23

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO. 2
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/381,488

FILING DATE: 11-P6b-2000

CLASSIFLATION: <university of the compatible of the compatibl
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ADDRESSE: BROWN, THERESA A.
STREET: 1560 Broadway, Suite 1200
CITY: Denver
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BROWN, THERESA A.
REGISTRATION NUMBER: 32,547
REFERENCE,DOCKET NUMBER: 41.
TELECOMMUNICATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibson, Helen L.
Fitzpatrick, Paul A.
Barr, Philip J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09381488
Patent No. 6441135
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863-0223
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-105-542A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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Sequence 7, Application US/08713000
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Patent No. 5789222
GENERAL INFORMATION
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FOR TILLE OF INVENTION:
FOR SEQUENCES:
CORRESPONDENCE ADDRESS:
GENERAL 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,716
FILING DATE: 23-JUN-1995
CLASSIFICATION:
NAME: KORSEN, ELLIOTT
REGISTRATION:
NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/POCKET NUMBER: 19453PV
TELECOMMUNICATION INFORMATION:
TELECHOME: 0908-594-5493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7e-09;
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1.2%; Score 47; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 47; Conservative 0; Mismatches 0;
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    LOCATION: 26.478

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-381-488-6
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: doubl
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STATE: NEW JERSEY
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NAME/KEY:
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MOLECULE TYPE:
HYPOTHETICAL: N
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LOCATION:
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RESULT 35 US-08-713-000-7

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Patent No. 595486

GENERAL INFORMATION:

APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.

TITLE OF INVENTION: MATERIALS AND METHODS FOR
ITILE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESSER: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
COUNTRY: USA
ZIP: 98121
COMPUTER PITT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1454;
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, 11kka
APPLICANT: Havukkala, 11kka
APPLICANT: GIVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                               Query Match
1.2%; Score 47; DB 2; L4
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Disketce
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SUSPTWARE: PascESQ for Windows Version 2.0
SUSPTWARE: WAS SUSPTEM: DOS
SUSPTWARE: WAS SUSPTEM: DOS
SUSPTWARE: WAS SUSPECTION DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGIEGRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1454 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-713-000-7
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                                                                                                                                                                                                           CITY: Seatt
STATE: WA
COUNTRY: U
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TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REPRENCE: 11000.1003-04U
CURRENT APPLICATION NUMBER: US 09/915,192A
CURRENT PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR PELING DATE: 1996-09-11
PRIOR PELING DATE: US 08/119,000
PRIOR FILING DATE: 1996-10-09
                                                                                                                                                                                                                                                                                                                 Length 1454;
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Lignin Content
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                                                                                                                                                                                                                                                                                                            Score 47; DB 4; L
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INCORPATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Likka
TITLE OF INVENTION: Materials and Methods for
TITLE OF INVENTION: Modification of Plant Lig
FILE REFERENCE: 11000.1003c2
CURRENT PRILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER PRILING DATE: 1997-11-21
EARLIER FILING DATE: 1997-11-21
EARLIER PILING DATE: 1996-09-11
SARLIER FILING DATE: 1996-09-11
SARLIER FILING DATE: 1996-09-11
SARLIER FILING DATE: 1996-09-11
SOFTWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                            Query Match
1.2%; Score 47; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 47; Conservative 0; Mismatches
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION: APPLICANT: Blokeberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09169789
Patent No. 6653528
                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-615-192A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-169-789-7
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                                                                                                                                                                                              LENGTH:
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GENERAL INFORMATION:

APPLICANT: Bloksberg, Leonard N.

APPLICANT: Havukkala, Ilkka

TITLE OF INVENTION: Materials and Methods for the

TITLE OF INVENTION: Modification of Plant Lignin Content

FILE REFERENCE: 11000.1003c4U

CURRENT APPLICATION NUMBER: US/09/615,192A

CURRENT FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Blokaberg, Leonard N.
APPLICANT: Blokaberg, Leonard N.
APPLICANT: Havukkala, 11kka
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c3
CURRENT APPLICATION NUMBER: US/09/211,710A
CURRENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
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1.6e-09;
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1.2%; Score 47; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                           11000/1003C1
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09211710A
Patent No. 6204434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09615192A Patent No. 6410718
                                                                                                                                       NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFRENCE/POCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7
SEQUEENCE CHARACTERISTICS:
LENGTH. 1454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-211-710-7
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1454
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Gaps

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/ Match
1.2%; Score 47; DB
Local Similarity 100.0%; Pred. No. 1.6
nes 47; Conservative 0; Mismatches
               FILING DATE:
CLASSIFICATION:
PHICK APPLICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/100
TELECOMMUNICATION INFORMATION:
TELEFRANS: 206-269-0565
TELEFRX: 206-26-0563
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Sequence 402, Application US/09615192A

Patent No. 6410718

GENERAL INFORMATION:

APPLICANT: Blokeberg, Leonard N.

APPLICANT: Havukkala, IIkka
  APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pinus radiata
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US-08-975-316-71
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Patent No. 5952486
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BLOKEBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003-22
CURRENT APPLICATION NUMBER: US 08/975,316
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER PILING DATE: 1996-09-11
NUMBER OF SEQ ID NOS: 185
SEQ ID NO 95
LENGTH: 1460
MATERIAL 1460

LENGTH: 1460
                                                                                                                                                                                                               0; Indels
                                                                                                                                                                    1.2%; Score 47; DB 4; Le
100.0%; Pred. No. 1.6e-09;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95, Application US/09169789
Patent No. 6653528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Pinus radiata
                                                                                 ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-615-192A-95
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                                                               1460
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US-09-169-789-95
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US-08-975-316-71
                    SOFTWARE: 1
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                                                                                                Sequence 71, Application US/09615192A
Sequence 71, Application US/09615192A
GENERAL INFORMATION:
APPLICANT: Blokeberg, Leonard N.
APPLICANT: Blokeberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content;
FILE REFERENCE: 11000.1003c4U
CURRENT FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 08/975,316
PRIOR PLICATION NUMBER: US 08/975,316
PRIOR PLILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 71
LENGTH: 1474
Query Match 1.2%; Score 47; DB 2; Length 1474; Best Local Similarity 100.0%; Pred. No. 1.6e-09; Matches 47; Conservative 0; Mismatches 0; Indels
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; Pred. No. 1.6e-09;
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1.2%; Score 47; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 4; L
Pred. No. 1.6e-09;
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APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 6/096,225
EARLIER APPLICATION NUMBER: 6/096,225
BARLIER OFFICH OFFICE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blokeberg, Leonard N.
APPLICANT: Blokeberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Madification of Plant Ligger Corresponding to the Presence: 11000.100312
FILE REPERENCE: 11000.100322
CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER FILING DATE: 1997-11-21
EARLIER FILING DATE: 1997-11-21
EARLIER FILING DATE: 1996-09-11
WUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                 Query Match
1.2%; Score 47; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 47; Conservative 0; Mismatches
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 71 LENGTH: 1474
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US-09-169-789-184
; Sequence 184, Application US/09169789
; Patent No. 6653528
; Patent INFORMATION:
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Patent No. 6297034
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-169-789-184
                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-169-789-71
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; ORGANISM: Oryza sativa
US-09-370-807-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2407
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develc
TITLE OF INVENTION: death and their use in the modification of forestry plant develc
TITLE OF INVENTION: death and their use in the modification of forestry plant develc
TITLE OF INVENTION: 208 CURRENT APPLICATION NUMBER: US/09/325,932A
UNMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 202
LENGTH: 1474
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                                          TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content; TITLE OF INVENTION: Modification of Plant Lignin Content; CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR PILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR PILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.2%; Score 47; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .6e-09;
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1.2%; Score 47; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-05
Matches 47; Conservative 0; Mismatches C
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Patent No. 6451604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-615-192A-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pinus radiata
US-09-325-932A-202
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US-09-325-932A-202
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US-09-169-789-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 402
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14761
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Best Local Similarity
Matches 46; Conserva
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Matches
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APPLICANT: BOGGET, Thierry
APPLICANT: BOGGET, Thierry
APPLICANT: BOGGET, Thierry
APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REPERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/845,917A
CURRENT FILIO DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 58
SOFTHAME: ALCENTION OF CELL BEHAVIOUR
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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100.0%; Pred. No. 1.4e-09;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2407;
  Length 2407;
Query Match 1.2%; Score 47; DE 3; Length 240
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0; Indels
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1.2%; Score 47; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               Sequence 7, Application US/09921259
Sequence 7, Application US/09921259
Patent No. 6465234
GENERAL INFORMATION:
APPLICANT: Calcon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Ballski, J. Antoni
APPLICANT: Ballski, J. Antoni
APPLICANT: Ballski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Ballski, J. 1998
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (8456)
OTHER INFORMATION: "N is A, C, G, or T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09845917A; Patent No. 6653529; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Oryza Bativa
US-09-921-259-7
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Best Local Similarity
Matches 47; Conservat
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LENGTH: 10288
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US-09-921-259-7
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                                                                                                                                                                                                APPLICANT: BOGBAST, Thierry
APPLICANT: BOGBAST, Thierry
APPLICANT: BOGBAST, Thierry
APPLICANT: Wandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
TITLE OF INVENTION: BY THE CONTROL OF CELL BEHAVIOUR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENT VERTICAL CONTROL OF CELL BEHAVIOUR
LENGTHAL 13414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: artificial OTHER INFORMATION: plasmid
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100.0%; Pred. No. 1.3e-09;
tive 0; Mismatches 0; Indels
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US-09-621-976-14761
US-09-621-976-14761
Sequence 14761, Application US/09621976
Sequence 14761, Application US/09621976
GENERAL INPORMATION:
APPLICANT: Under M. S. APPLICANT: Uobert, S. APPLICANT: Uobert, S. TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTMARE: Patent.pm
SEQ ID NO 14761
LENGTH: 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/FEX: misc_feature
LOCATION: (11582)
OTHER_INFORMATION: "N is A, G, C or T"
                                                                                                                                    US-09-845-917A-27/c
; Sequence 27, Application US/09845917A
; Patent No. 6653529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: FUNCES, TOWN
APPLICANT: Vedvick, Town
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478015
CURRENT PILING DATE: 2000-12-13
CURRENT PILING DATE: 2000-12-13
SOFTWARE: FastSEQ for Windows Version 3.0
; EQ. 10 NO.12.
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Patent No. 6630574

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodges, Michael A.
APPLICANT: Lodges, Michael A.
APPLICANT: Panger, Garry
APPLICANT: Catter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 199;
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1.2%; Score 46; DB 4; L
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0;
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1.2%; Score 46; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0;
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         Wang, Tongrous
Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapien
US-09-614-124B-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapien
US-09-736-457-102
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US-09-614-124B-102
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US-09-671-325-102
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LENGTH: 199
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Patent No. 6504010

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Eanger, Chaiteanya S.
APPLICANT: Fanger, Gary
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc
APPLICANT: Constant Consoling Conso
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                                                                                                         GENERAL INCORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054R2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 10543
LENGTH: 193
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1.2%; Score 46; DB 4; L.
Best Local Similarity · 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0;
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                                Sequence 10543, Application US/09621976
Patent No. 6639063
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; Sequence 102, Application US/09736457
; Patent No. 6509448
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1 LOCATION: 36..37

2 OTHER INFORMATION: n=a, g, c or t

US-09-621-976-10543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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CRGANISM: Homo Bapien
US-09-702-705-102
JS-09-621-976-10543
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Score 46; DB 4; L
Pred. No. 4.9e-09;
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1.2%; Score 46; DB
Best Local Similarity 100.0%; Pred. No. 4.9
Matches 46; Conservative 0; Mismatches
TITLE OF INVENTION: ESTS and Encoded Human.
FILE REFERENCE: GENSET 054PR2
CURRENT PELLIANG NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16536
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-621-976-16317; Application US/09621976; Sequence 16317, Application US/09621976; Patent NO. 6639063; GENERAL INPORMATION: APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-16317
                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-16536
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: 231
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LENGTH: 235
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                                                       APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodges, Michael A.
APPLICANT: Lodges, Michael A.
APPLICANT: Panger, Gary
APPLICANT: APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: MANNION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAZATON NUMBER: US/09/589,184
FILE REFERENCE: 210121.47808
CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT PILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: FastSEQ for Windows Version 3.0
INVENTION 102
SEQ ID NO 102
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Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
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1.2%; Score 46; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0;
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Sequence 16536, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 102, Application US/09589184 Patent No. 6686447 GENERAL INFORMATION:
            angur, Chaitanya S.
odes, Michael A.
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US-09-589-184-102
                                                                                                                                                                                                                                                                                                                                                                                                                   , TYPE: DNA
, ORGANISM: Homo sapien
US-09-671-325-102
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1.2%; Score 46; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
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Patent No. 6639063;
GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JODERT, S.
APPLICANT: Glordano, J.Y.
ITILE OP INVENTION: ESTS and Encoded Human Proteins.;
FILE REPERENCE: GENER. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OP SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: BSTB and Encoded Human Proteins. FILE REFERENCE: GENSET. 054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NO 16317 LENGTH: 231
and Encoded Human Proteins.
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Best Local Similarity 100.0
Matches 46; Conservative
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CORGANISM: Homo sapiens
US-09-621-976-16291
                                                                                                                                                                                                                              rYPE: DNA COGGANISM: Homo sapiens US-09-621-976-16288
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LENGTH: 249
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                                                                                                            Query Match
1.2%; Score 46; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
                                        Length 235;
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                                                                            0; Indels
                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
VUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1634, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johner M. 3.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                    Query Match
1.2%; Score 46; DB 4; Ls Best Local Similarity 100.0%; Pred. No. 4.8e-09; Matches 46; Conservative 0; Mismatches 0;
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100.0%; Pred No. 4.8e-0
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Mismatches
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US-09-621-976-16320
; Sequence 16320, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
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US-09-621-976-16288
; Sequence 16288, Application US/09621976
; Patent No. 6639063
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Best Local Similarity 100.0%; P.
Matches 45; Conservative 0;
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SOFTWARE: Patent.pm
SEQ ID NO 16324
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-621-976-16320
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US-09-621-976-9455
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LENGTH: 242
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APPLICANT: Jobert, S.
APPLICANT: Glocit, S.
TITLE OF INVENTION: ESTR and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 1688
LENGTH: 246
TYPE: No.
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PAEINT.PM
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1.2%; Score 46; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 46; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4.8e-09;
iive 0; Mismatches 0;
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 16292
LENGTH: 249
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; Sequence 16291, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION;
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US-09-621-976-16581

Sequence 16581, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Unuas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET .054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 16581

ERNOTH: 356
       APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18648
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16999, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Unas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INFORMATION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

LENGTH: 283
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Pred. No. 4.7e-09;
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Dumas Milne Edwards, J.B.
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US-09-621-976-16989
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo (
US-09-621-976-18648
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US-09-621-976-16989
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                                                                                     Query Match 1.2%; Score 46; DB 4; Length 259; Best Local Similarity 100.0%; Pred. No. 4.8e-09; Matches 46; Conservative 0; Mismatches 0; Indels
               Length 249;
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US-09-621-976-18893
US-09-621-976-18893
Sequence 18893, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTA and Encoded Human Proteins.
FILE REFERENCE: GENSET.054F2
CURRENT FILIG DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 18893
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16294, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Minne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Goldano, J.Y.
ITTLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOCTWARRE: Patent.pm
SEQ ID NO 16594
LENGTH: 259
             1.2%; Score 46; DB 4; L4
100.0%; Pred. No. 4.8e-09;
iive 0; Mismatches 0;
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1.2%; Score 46; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 46; Conservative 0; Mismatches 0;
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                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Homo sapiens
US-09-621-976-16294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRGANISM: Homo sapiens US-09-621-976-18893
                               Local Similarity
les 46; Conser
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US-09-621-976-16294
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US-09-621-976-18648
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               Query Match
                                   Best Loc
Matches
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Gaps

, LOCATION: 230..231

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Gaps
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Patent No. 6660907
GENERAL INFORMATION:
APPLICANT: Hendrick, Carol A
APPLICANT: Hu, Xu
APPLICANT: Lu, Guihua
TITLE OF INVENTION: GENES ENCODING SCIP-1 ORTHOLOGS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 46; Conservative 0; Mismatches 0;
                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1.US
                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILLING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER APPLICATION NUMBER: 60/048,187
EARLIER FILLING DATE: 1997-05-30
EARLIER FILLING DATE: 1997-05-30
EARLIER FILLING DATE: 1997-06-52
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATCHIN OF: 2.0
SEQ ID NO 26
LENGTH: 700
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J. LOCATION: (700)
J. CTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-26
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LOCATION: (692)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (659)
OTHER INFORMATION:
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| Sequence 186, Application US/09220132 |
| Sequence 186, Application US/09220132 |
| Sequence 186, Application US/09220132 |
| Patent No. 6506607 |
| General Information: Andrew W. |
| TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT |
| TITLE OF INVENTION: MARK: US/09/220,132 |
| CURRENT APPLICATION NUMBER: US/09/220,132 |
| CURRENT PILING DATE: 1998-12-23 |
| PRIOR FILING DATE: 1998-12-23 |
| PRIOR FILING DATE: 1998-03-25 |
| PRIOR FILING DATE: 1998-12-24 |
| NUMBER OF SEQ ID NOS: 191-24 |
| SEQ ID NO 186 |
| SEQ ID NO 186 |
| LENGTH: 495 |
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                                                                                                                                                                                                                                Length 399;
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                                                                                                   Length 356;
                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9484, Application US/09621976

Batent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITILE OF INTENTION: STF and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION MUMBER: US/09/621,976
CURRENT FILING DATE: 2000.07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Ratent.pm
SEQ ID NO 9484
LENGTH: 399
                                                                                            Query Match
1.2%; Score 46; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 46; Conservative 0; Mismatches 0;
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1.2%; Score 46; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 46; Conservative 0; Mismatches 0;
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Pred. No. 4.5e-09;
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; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-16581
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Best Local Similarity 100.0
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-09-621-976-9484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
COGANISM: Homo sapiens
US-09-220-132-186
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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, LOCATION:
US-08-197-793-1
        COUNTRY:
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APPLICANT: Mener, S.
APPLICANT: Schoenhaut, D.
APPLICANT: Retnofsky, S.
TILE OF INVENTION: pp32: A Newly Identified CD45-Associated
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 46; DB 4; Length 776; 100.0%; Pred. No. 4.3e-09; Live 0; Mismatches 0; Indels
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US-09-621-976-2725

Sequence 2725, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERT: 054PR2
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NOS 2725

LENGTH: 890
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Pred. No. 4.3e-09;
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1.2%; Score 46; DB
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 46; Conservative 0; Mismatches
FILE REFERENCE: 035718/236026 (5718-129)
CURRENT APPLICATION NUMBER: US/09/902,3318
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,156
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: LAHIVE & COCKFIELD
60 STATE STREET, SUITE 510
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Patent No. 5510461
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 46; Conservative
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                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(606)
US-09-902-331B-3
                                                                                                                                SEQ ID NO 3
LENGTH: 776
TYPE: DNA
ORGANIEM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: 333..683
US-09-621-976-2725
                                                                                                                                                                                                                                                                                                         Query Match
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278: ONDERTER READABLE FORM; 148.

COMPATTER APPLICATION NOTA:

APPLICATION NOTE:

APPLICATION NOT
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Gaps
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                                                                                  Query Match
1.2%; Score 46; DB 5; Length 953;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZO44P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
SEQ ID NOS: 217
SOFTWARE: PALENTIN NUMBER: 60/155,709
FRIOR FILING DATE: 1999-09-24
SEQ ID NOS: 217
SEQ ID NO 14
LENGTH: 997
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1.2%; Score 46; DB 4; Li
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 46; Conservative 0; Mismatches 0;
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Facent No. 6410709
FILE REFERENCE: POSISPI
CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
FARLIER PILING DATE: 1999-08-29
FARLIER FILING DATE: 1997-08-29
FERLIER APPLICATION NUMBER: 60/056,271
FARLIER APPLICATION NUMBER: 60/056,271
FARLIER APPLICATION NUMBER: 60/056,271
FARLIER RILING DATE: 1997-08-29
FARLIER POPILCATION NUMBER: 60/056,073
FARLIER POPIL CATION NUMBER: 60/056,073
FARLIER POPINGE: 128
FARLIER POPINGE: 128
FARLIER POPINGE: 128
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; Sequence 14, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-800-729-14
               PCT-US95-01618-1
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TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STRTE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 953;
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APPLICATION NUMBER: 07/688,019; 08/004,199
FILING DATE: 19-APR-1991; 13-JAN-1993
ATTORNEY, PARTITIONERMATION:
NAME: DeCONTI, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-006CNCP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.7) 227-7400
TELEPHONE: (6.7) 227-740
TELEPHONE: (6.7) 227-740
TELEPHONE: (6.7) 227-75941
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 953 base pairs
TERNTE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE PORM:

COMPUTER READABLE PORM:

COMPUTER: ISM PC compatible

COMPUTER: ISM PC compatible

COMPUTER: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01618

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION:

RAPLICATION NUMBER: USSN 08/197,793

ATTORNEY/AGENT INFORMATION:

NAME: Deconti, Giulio A., Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-006CPPC

TELECOMMUTICATION INFORMATION:

TELECOMMUTICATION INFORMATION:

THE COMPATION TREPERS IN THE COMPATION:

THE COMPATION TREPERS INFORMATION:

THE COMPATION TREPERS INFORMATION TREPERS
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GENERAL INFORMATION:
APPLICANT:
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 953 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
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64..681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 64..681
US-08-636-176-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
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LOCATION:
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GENERAL INCORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 32 Human secreted proteins;
FILE REFERENCE: PZO44P1

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: PCT/US00/26013

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR PELICATION NUMBER: 60/155,709

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SOFFWARE: Autentin Ver. 2.0
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Sequence 44, Application US/09800729

Sequence 44, Application US/09800729

Sequence 44, Application US/09800729

Sequence 44, Application US/09800729

GENERAL INFORMATION:

TILLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT PELING DATE: 2001-03-08

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR APPLICATION NUMBER: 60/155,709

SOFTWARE: PATENT 1138

SEQ ID NOS: 217

SEQ ID NO 44

LENGTH: 1138
                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 4; Le Pred. No. 4.2e-09;
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Pred. No. 4.2e-09;
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TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR PRILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 4.2
Matches 46; Conservative 0; Mismatches
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Patent No. 6605592
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-44
                                                                                                                                                                                                                                                                 SEQ ID NO 48
LENGTH: 1086
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                        Query Match 1.2%; Score 46; DB 4; Length 1071; Best Local Similarity 100.0%; Pred. No. 4.2e-09; Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1039;
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                                                                                                             US-09-464-535-23
US-09-464-535-23
i Sequence 23, Application US/09464535
i Petent No. 6545200
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafaleki, J. Antoni
ITIE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1306 US NA
CURRENT FILING DATE: 1999-12-15
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Microsoft Office 97
SEQ ID NO 23
LEMGTH: 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/09800729
Patent No. 660552
GENERAL INFORMATION:
JITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PC044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR PLILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 45
LENGTH: 1071
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US-09-800-729-48
, Sequence 48, Application US/09800729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-464-535-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-800-729-45
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US-09-800-729-45
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Gaps

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A PELLING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22
RR APPLICATION NUMBER: 60/056,893
ER FILING DATE: 1997-08-22
ER PILING DATE: 1997-08-22
                                                                                                           EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER PILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043, 313
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER PELICATION NUMBER: 60/043, 315
EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER PELING DATE: 1997-06-06
EARLIER PELING DATE: 1997-06-06
EARLIER PELING DATE: 1997-06-22
EARLIER APPLICATION NUMBER: 60/056, 886
EARLIER APPLICATION NUMBER: 60/056, 887
EARLIER APPLICATION NUMBER: 60/056, 893
EARLIER APPLICATION NUMBER: 60/056, 893
EARLIER FILING DATE: 1997-08-22
EARLIER PELING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
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APPLICATION UNDBER: 60/043,313
ELING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
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APPLICATION UNDRER: 60/056,911
APPLICATION DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
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1.2%; Score 46; DB 4; Length 114
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
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FULL REFERENCE: P2002P1
FULL REFERENCE: P2002P1
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
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R FILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
R APPLICATION NUMBER: 60/047,633
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,583
R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,615
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Patent No. 6420526
GENERAL INFORMATION:
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; NUMBER OF SEQ ID NOS: 217; SOFTWARE: Patentin Ver: 2.0; SEQ ID NO 47; LENGTH: 1149; TYPE: DNA; ORGANISM: Homo sapiens US-09-800-729-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE:
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US-09-149-476-41
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(G DATE: 1997-04-11
(CATION NUMBER: 60/043,576
MG DATE: 1997-04-11
ICATION NUMBER: 60/047,501
MG DATE: 1997-05-23,
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JATION NUMBER: 60/056,876
PATE: 1997-08-22
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PLICATION NUMBER: 60/056,881
LING DATE: 1997-08-22
PLICATION NUMBER: 60/056,909
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TENT NATE: 1997-08-22
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PPLICATION NUMBER: 60/048,964
PLIC DATE: 1997-06-06
PPLICATION NUMBER: 60/057,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FULCALION NUMBER: 60/056,884
PPLICATION NUMBER: 60/056,884
                                                                                                                                                                                                                                                        LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,590
LING DATE: 1997-05-23
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ATION NUMBER: 60/047,614
NATE: 1997-05-23
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ATION NUMBER: 60/056,632
DATE: 1997-08-22
ATION NUMBER: 60/056,664
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PLICATION NUMBER: 60/056,908
LING DATE: 1997-08-22
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3 DATE: 1997-09-05
APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,761
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ZATION NUMBER: 60/043,670
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PLICATION NUMBER: 60/056,862
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PLICATION NUMBER: 60/056,887
                                                                                                                  CATION NUMBER: 60/047,599
                                                                                                                                     LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,588
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                                                                             /047,595
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                                                      0; Indels
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TILLE OF INVENTION: 207 Human Secreted Proteins
FILLE REFERENCE: P2007P1
CURRENT FILING DATE: D2007P1
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: P2007 P1
EARLIER PILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,000
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100.0%; Pred. No. 4.1e-09;
tive 0; Mismatches 0;
  Query Match
1.2%; Score 46; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Call, Joan T.
APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Cathenine J.
APPLICANT: Thorpe, Cathenine J.
APPLICANT: Thorpe, Cathenine J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: STEROL METABOLISM ENZYMES
FILE REFERENCE: BB1114 US NA
CURRENT APPLICATION NUMBER: US/09/439,554
CURRENT FILING DATE: 1999-11-12
EARLIER APPLICATION NUMBER: 60/108,351
EARLIER PILING DATE: 1999-No. 6479733ember-13
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 23
LENGTH: 1192
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
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Patent No. 6525174
                                                                                                                                                                                                                                                                             US-09-439-554-23
; Sequence 23, Application US/09439554
? Patent No. 6479733
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 46; Conservative
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CORGANISM: Glycine max
US-09-439-554-23
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Patent No. 625838

Patent No. 625838

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

FILE REFRENCE: MNI-051

CURRENT APPLICATION NOWBER: US/09/164,193C

CURRENT FILING DATE: 1998-09-30

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 1315
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                                                                                                                                                                                                                                                                   APPLICANT: O'GENTE, BRIAN
APPLICANT: O'GER, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
BARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 25
LENGTH: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS

) LOCATION: (249)...(767)

) FRATURE:

) OTHER INSEMMATION: 'n' at position 1315 may be any nucleotide

US-09-164-193-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2%; Score 46; DB 3; Length 1279; Best Local Similarity 100.0%; Pred. No. 4.1e-09; Matches 46; Conservative 0; Mismatches 0; Indels
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1.2%; Score 46; DB 3; Length 1315;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                      RESULT 90
US-09-248-315-25
US-09-248-315-25
; Sequence 25, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION
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Parent No. 643668
GENERAL INFORMATION:
APPLICAINT: ACCON, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: maize US-09-248-335-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-221-448A-1
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US-09-164-193-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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100.0%; Pred. No. 4.1e-09;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER PILLING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PREDICCATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER PREDICCATION NUMBER: 60/048,963
EARLIER PREDICCATION NUMBER: 60/048,973
EARLIER PREDICCATION NUMBER: 60/048,973
EARLIER PREDICCATION NUMBER: 60/048,973
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-07-05-06
EARLIER PILING DATE: 1998-07-05
EARLIER PILING DATE: 1998-07-05
SEQITWARE: PAPELICATION NUMBER: 60/094,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,970
ER PILING DATE: 1997-06-06
ER APLICATION NUMBER: 60/048,972
ER FILING DATE: 1997-06-06
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/049,313
ERILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/049,373
ERILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,373
ERILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,375
ERILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,019
                                                                                                              FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,882
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,899
                                                                                                                                                                                                                                                                                      FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
PELICATION NUMBER: 60/048,901
FILING DATE: 1997-06-06
                                                                                  PLICATION NUMBER: 60/048,971
      FILING DATE: 1997-06-06
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Best Local Similarity 100
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-25
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EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-606
EARLIER FILING DATE
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TITLE OF INVENTION: NOVEL CSAPTP PROTEIN MOLECULES AND USES THEREFOR (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: CDS

LOCATION: (249)..(767)

COTHER INFORMATION: 'n' at position 1315 may be any nucleotide US-09-221-448A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 4; Length 1315;
Pred. No. 4.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208, Application US/09149476
| Sequence 208, Application US/09149476
| Patent No. 6420526
| Patent No. 6420526
| GENERAL INPORMATION: 186 Human Secreted proteins FILIE REFERENCE: P26002P1
| TILLE PERFENCE: P26002P1
| CURRENT FILING DATE: 1998-03-06
| EARLIER PILING DATE: 1998-03-06
| EARLIER PILING DATE: 1997-03-07
| EARLIER APPLICATION NUMBER: 60/040,162
| EARLIER APPLICATION NUMBER: 60/040,162
| EARLIER APPLICATION NUMBER: 60/040,163
| EARLIER APPLICATION NUMBER: 60/040,162
| EARLIER APPLICATION NUMBER: 60/040,163
| EARLIER APPLICATION NUMBER: 60/040,626
| EARLIER APPLICATION NUMBER: 60/040,626
| EARLIER APPLICATION NUMBER: 60/040,626
| EARLIER APPLICATION NUMBER: 60/040,636
| EARLIER FILING DATE: 1997-03-07
| EARLIER APPLICATION NUMBER: 60/047,633
| EARLIER PILING DATE: 1997-05-23
| EARLIER APPLICATION NUMBER: 60/047,633
| EARLIER PILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 46; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 46; Conservative 0; Mismatches
                                FILE REFERENCE: MNI-051DV1
CURRENT APPLICATION NUMBER: US/09/221,448A
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1315
                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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RAKLIER FILING DATE: 1997-08-22

RAKLIER FILING DATE: 1997-08-23

RAKLIER FILING DATE: 1997-08-23

RAKLIER FILING DATE: 1997-08-23

RAKLIER FILING DATE: 1997-08-23

RAKLIER PAPLICATION NUMBER: 60/047, 595

RAKLIER PAPLICATION NUMBER: 60/047, 596

RAKLIER RAPLICATION NUMBER: 60/047, 596

RAKLIER RAPLICATION NUMBER: 60/047, 591

BARLIER RAPLICATION NUMBER: 60/056, 891

BARLIER RILING DATE: 1997-08-25

BARLIER FILING DATE: 1997-08-25

BARLIER FILING DATE: 1997-08-25

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1.2%; Score 46; DB 4; Length 1477;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                           Length 1378;
                                                                                                                                                                               0; Indels
                                                                                                                                         Query Match
1.2%; Score 46; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Butler, Karlene
APPLICANT: Butler, Karlene
APPLICANT: Butler, Karlene
APPLICANT: Gutteridge, Steven
APPLICANT: Gutteridge, Steven
TILE REPERBACE: BB1370 US NA
CURRENT APPLICATION NUMBER: US/09/585,173B
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US/09/585,173B
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS? 54
SEQ ID NO 7
LENGTH: 1477
TYPE: DNA
TYPE: DNA
             EARLIER APPLICATION NUMBER: 60/057,669
EARLIER PILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 220, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09585173B
Patent No. 6570063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
FILING DATE: 1997-06
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 95
US-09-907-794A-220
                                                                                                                                                                                                                                                                                                                                US-09-585-173B-7
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILE REFERENCE: 10466-14

CURRENT PAPLICATION NUMBER: US/09/905,125A

CURRENT PAPLICATION NUMBER: US/09/905,125A

PRIOR APPLICATION NUMBER: US/01/12

PRIOR PILING DATE: 2000-02-22

PRIOR FILING DATE: 1099-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-03

PRIOR PRIOR DATE: 1999-12-03

PRIOR PRIOR DATE: 
                                                                                                                                                                                                    Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                          Gurney, Austin L.
Hillan, Kenneth, J
                                                                                                   Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
Filvaroff, Ellen
                             ong, Suc.
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; ORGANISM: Homo sapiens
US-09-905-125A-220
                                                                                                                                                                      Soddard, A.
                             APPLICANT: RCY, MALSH-L.

APPLICANT: RCAV, MALSH-L.

APPLICANT: Thuns, Daniel

APPLICANT: Thuns, Daniel

APPLICANT: Thuns, Daniel

APPLICANT: Wood, Milliam, I.

TITLE OF INVENTION. Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION. Acids Encoding the Same

CURRENT APPLICATION WUMBER: US/99/907,794A

CURRENT FILING DATE: 2000-00-22

CURRENT PRIOR DATE: 1090-00-22

PRIOR PALLICANION WUMBER: DC/144.048

PRIOR PALLICANION WUMBER: US/0144.048

PRIOR PALLICANION WUMBER: US/0146.222

PRIOR PALLICANION WUMBER: US/0146.222

PRIOR PALLICANION WUMBER: PCT/US99/20594

PRIOR PALLICANION WUMBER: PCT/US99/20594

PRIOR PALLICANION WUMBER: PCT/US99/20694

PRIOR PALLICANION WUMBER: PCT/US99/20694

PRIOR PALLICANION WUMBER: PCT/US99/2069

PRIOR PALLICANION WUMBER: PCT/US99/3091

PRIOR PALLING DATE: 1999-12-20

PRIOR PALLING DATE: 
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100.0%; Pred. No. 4e-
trive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 46; Conservative
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US-09-905-125A-220
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Ferrara, Napoleone

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botterin, David
APPLICANT: Benoyers, Luc
APPLICANT: Baton, Dan L.

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15-02-820-004-1
Sequence 1, Application US/09820004
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES TITLE OF INVENTION: THEREOF PLOSE OF TILE REFERENCE: CLOOL201
CURRENT APPLICATION NUMBER: US/09/820,004
CURRENT PILLING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 6
SOCTHARR: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1606
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TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
FILE REFERENCE: PF391
CURRENT APPLICATION NUMBER: US/09/244,111
CURRENT FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 60/073,961
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1527
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                                                                                                                    Length 1503;
                                                                                                                                                                          Indels
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1.2%; Score 46; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4e-09;
Matches 46; Conservative 0; Mismatches 0;
                                                                                                              ch 1.2%; Score 46; DB 4; Le
1 Similarity 100.0%; Pred. No. 4e-09;
46; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09244111 Patent No. 656498 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-220
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LOCATION: (67)..(1335)
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; ORGANISM: Human
US-09-820-004-1
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US-09-244-111-7
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PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: DCT/USO0/04114
PRIOR FILING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
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PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
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PLICATION NUMBER: US/09/902,775A
LING DATE: 2001-07-10
                                                                                        Sequence 220, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Mather, Jennie P.
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ao, Wei-Qiang
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Tumas, Daniel
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CURRENT APPLICA
CURRENT FILING
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Search completed: April 23, 2004, 08:26:47 Job time : 249 secs

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Sequence 140, Applisequence 11, Applisequence 13, Applisequence 31, Applisequence 31, Applisequence 31, Applisequence 6158, Apsequence 6158, Apsequence 6158, Apsequence 6158, Apsequence 6158, Apsequence 61519, Applisequence 61519, Applisequence 39, Applisequence 3
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10 US-10-436-523-41139

10 US-10-424-599-46733

10 US-10-219-464-39

10 US-10-219-464-39

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                                                                                                                            April 23, 2004, 08:22:52 ; Search time 1469 Seconds (without alignments) 11546.259 Million cell updates/sec
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US-10-10-6-698-70

US-09-925-301-10

5 US-10-198-46-971

5 US-10-424-599-11755

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APPLICANT: Union Chimique Belge, S.A. APPLICANT: No. US200301668B1A1ka, Karl APPLICANT: Pirozzi, Gregory APPLICANT: Pirozzi, Gregory APPLICANT: Binstein, Richard TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST CEI TITLE OF INVENTION: ACTIVATION FILE REPERENCE: 053520-5005 CURRENT APPLICATION UNMER: US/10/005,907 CURRENT PILING DATE: 2001-12-07 NUMBER OF SEQ ID NOS: 13 SOFTWARE: Patentin version 3.1 LENGTH: 3762 TYPE: DNA CREANIEM: RAME/KEY: CDS MAME/KEY: CDS MAME/KEY	Query Match 100.0%; Score 3762; DB 15; Length 3762; Best Local Similarity 100.0%; Pred. NO.0; Mismatches 0; Indels 0; Gaps 0; QY 1 GAGAACCGAGTCACTGTGAAAAGATGACCAAAACTCAGTTGCCTG 60 1 GAGAAACCGAGTCACTGTGAAAAGATTATCTCCTGCGAAAACTCAGTTGCCTG 60 QY 61 GGAGAGAATCAAAAGAAAGAAAAGAAAACTCAGGAAAACTCAGTTGACGAAAACTCAGGAAACTCAGAAAACTCAGAAAACAAAAAAAA	ACTICIDATION CONTROLL	421 481 481 541 601 601
88 48 1.3 1837 15 US-10-219-077-39 Sequence 39, Appl 89 48 1.3 1837 15 US-10-219-465-39 Sequence 39, Appl 90 48 1.3 1837 15 US-10-219-465-39 Sequence 39, Appl 91 48 1.3 1837 15 US-10-219-465-39 Sequence 39, Appl 92 48 1.3 1837 15 US-10-219-473-39 Sequence 39, Appl 93 48 1.3 1837 15 US-10-219-473-39 Sequence 39, Appl 95 48 1.3 1837 15 US-10-219-476-39 Sequence 39, Appl 97 48 1.3 1837 15 US-10-219-482-39 Sequence 39, Appl 97 48 1.3 1837 15 US-10-227-876-39 Sequence 39, Appl 98 48 1.3 1837 15 US-10-227-876-39 Sequence 39, Appl 100 48 1.3 1837 15 US-10-229-974-39 Sequence 39, Appl 101 48 1.3 1837 15 US-10-229-974-39 Sequence 39, Appl 102 48 1.3 1837 15 US-10-229-974-39 Sequence 39, Appl 103 48 1.3 1837 15 US-10-220-113-39 Sequence 39, Appl 104 48 1.3 1837 15 US-10-230-139 Sequence 39, Appl 104 48 1.3 1837 15 US-10-230-306-39 Sequence 39, Appl 105 48 1.3 1837 15 US-10-230-306-39 Sequence 39, Appl 106 48 1.3 1837 15 US-10-230-306-39 Sequence 39, Appl 106 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 106 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 106 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-230-43-39 Sequence 39, Appl 107 48 1.3 1837 15 US-10-23	48 1.3 1837 15 US-10-230-435-39 Sequence 39, 48 1.3 1837 15 US-10-230-438-39 Sequence 39, 48 1.3 1837 15 US-10-232-222-39 Sequence 39, 48 1.3 1837 15 US-10-219-070-39 Sequence 39, 48 1.3 1837 15 US-10-219-070-39 Sequence 39, 48 1.3 1837 15 US-10-219-65-39 Sequence 39, 48 1.3 1837 15 US-10-216-166-39 Sequence 39, 48 1.3 1837 15 US-10-216-166-39 Sequence 39, 48 1.3 1837 15 US-10-216-163-39 Sequence 39, 48 1.3 1837 15 US-10-218-765-39 Sequence 39, 48 1.3 1837 15 US-10-218-765-39 Sequence 39, 48 1.3 1837 15 US-10-219-066-39 Sequence 39, 48 1.3 1837 15 US-10-219-069-39 Sequence 39, 48 1.3 1837 15 US-10-2	48 1.3 1837 15 US-10-219-475-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-480-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-480-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-528-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-528-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-530-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-531-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-532-39 Sequence 39, App. 48 1.3 1837 15 US-10-219-533-39 Sequence 39, App. 48 1.3 1837 15 US-10-232-228-39 Sequence 39, App. 48 1.3 1831 13 US-10-232-228-39 Sequence 39, App. 48 1.3 3010 13 US-10-232-224-7 Sequence 7, Appl. 48 1.3 3010 13 US-10-232-224-7	48 1.3 3010 15 US-10-227-884-7 Sequence 7, 48 1.3 3010 15 US-10-230-163-7 Sequence 7, 48 1.3 3010 15 US-10-230-163-7 Sequence 7, 48 1.3 3010 15 US-10-230-338-7 Sequence 7, 48 1.3 3010 15 US-10-218-631-7 Sequence 7, 48 1.3 3010 15 US-10-218-159A-7 Sequence 7, 48 1.3 3010 15 US-10-216-159A-7 Sequence 7, 48 1.3 3010 15 US-10-216-159A-7 Sequence 7, 48 1.3 3010 15 US-10-227-883-7 Sequence 7, 5 US-10-227-883-7 Sequence 7, 8 US-10-227-883-7 Sequence 7, 9 US-1

RESULT 1
US-10-005-907-1
; Sequence 1, Application US/10005907
; Publication No. US20030166881A1
; GENERAL INFORMATION:

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                                                                                                FEATURE:

NAME/KEY: unsure

COCATION: (1)..(261)

OTHER INFORMATION: unsure at all n locations
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_99145C.1
US-10-424-599-141898
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1.3%; Score 50; DB 13; I
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 50; Conservative 0; Mismatches 0;
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| NAME/KEY: misc feature
| LOCATION: (1694)
| OTHER INPORMATION: n equals a,t,g, or NAME/KEY: misc feature
| LOCATION: (1696)
| COTHER INPORMATION: n equals a,t,g, or US-09-925-300-395
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Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Anonahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141898
LENGTH: 261
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                                                              TYPE: DNA ORGANISM: Glycine max
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US-09-925-300-395
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US-10-171-311-67
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US-10-44-599-141898
US-10-44-599-141898
NS-10-44-599-141898
Sequence 141898, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Care Younged
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3001 GETTAATAACAGTATTGATTGGTAGAAGGAACGTTGAAATCCAAGAGCATCAATGTCTT
                                                                                                                                                                                                                 CTGGTGGTTCACCATAAGCCACAGCAGATGTCTTAATCTTTCCGAGATCTAGTTTTTCAG
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TILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides FILE REFERENCE: PA005P1

TILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR APPLICATION NUMBER: US 60/163,280
                                                                    APPLICANT: About the APPLICANT: Cao Yongwei TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53223) B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 606
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NAME/KEY: unsure

LOCATION: (1)...(606)

OTHER INFORMATION: unsure at all n locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_131628C.1

US-10-424-599-35023
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1.3%; Score 49; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 49; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 741, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
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Patent No. US20020052308Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-10-106-698-741
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US-09-925-301-10
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APPLICANT: Salceda, Susana
APPLICANT: Salceda, Roberto
APPLICANT: Macina, Roberto
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
FILE REPREMENTS: DEX.-02.67
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
HILLO OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDEATIFICATION, ASSESSMENT, PREVENTION, AND THERAPY ITLE OF INVENTION: OF CERVICAL CANCER TITLE OF INVENTION: OF CERVICAL CANCER CURRENT APPLICATION NUMBER: US 10/10/11,311
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-16-13
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PASISEQ for Windows Version 4.0
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1.3%; Score 50; DB 15; Length 3602;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 50; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/249,992
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
SOFTWARE: Patentin version 3.1
SEQ ID NO 87
PENGTH: 476
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Publication No. US20020132255A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 2087, 2093, 2098
COTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-001-843-87
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: And Vihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (55223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 11755
LENGTH: 1417
                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT3847_110622C.1
US-10-424-599-11755
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US-10-424-599-106798
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Pred. No. 1.1e-11;
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illarity 100.0%; Pred. No. 1.1
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: YIENS, PATRICE
APPLICANT: FERT, VINCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Glycine max
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PREVENTION, AND
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1.3%; Score 49; DB 15; Length 1392;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 49; Conservative 0; Mismatches 0; Indels
                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT PILITHO DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,301
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1373;
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100.0%; Pred. No. 1.1e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9741, Application US/10198846
| Publication No. US2003009974A1
| GENERAL INPORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Xu, Yongyao
| APPLICANT: Xi, Yongyao
| APPLICANT: Steinman, Kathleen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KI
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| FILE REFERENCE: MRI-049
| CURRENT APPLICATION NUMBER: US/10/198,846
| CURRENT APPLICATION NUMBER: 60/306,220
| FRIOR APPLICATION NUMBER: 60/306,220
| RAIOR APPLICATION NUMBER: 60/306,220
| NUMBER OF SEQ ID NOS: 14084
| SOSTWARRE: PSECEEC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (1364)
CTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1373)
CTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-10
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 49; Conservative
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; ORGANISM: Homo sapiens
US-10-198-846-9741
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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US-10-198-846-9741/c
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Sequence 106798, Application US/10424599
Publication No. US2004001072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cou Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEG ID NOS: 285684
SEQ ID NO 106798
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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1.3%; Score 49; DB 13; Length 1417;
100.0%; Pred. No. 1.1e-11;
tive 0; Mismatches 0; Indels (
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APPLICATION NUMBER: 60/241,785
FILING DATE: 2000-10-20
FILING DATE: 2000-10-20
FILING DATE: 2000-11-01
APPLICATION NUMBER: 60/244,617
APPLICATION NUMBER: 60/225,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 2000-07-26
APPLICATION NUMBER: 60/241,809
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLING DATE: 2000-08-14
PPLICATION NUMBER: 60/236,368
TLING DATE: 2000-09-29
PPLICATION NUMBER: 60/251,856
ILING DATE: 2000-12-08
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FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
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PPLICATION NUMBER: 60/234,997
ILING DATE: 2000-09-25
                            APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/217,496
                                                                                             FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
                                                                                                                                         FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
APPLICATION OWBER: 60/225,757
                                                                                                                                                                                                                                  LING DATE: 2000-08-14
PLICATION NUMBER: 60/226,868
                                                                                                                                                                                                                                                                           TILING DATE: 2000-08-22
TEPLICATION NUMBER: 60/216,647
TEPLICATION NUMBER: 60/216,547
APPLICATION NUMBER: 60/225,267
                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 2000-08-14
PLICATION NUMBER: 60/216,880
LING DATE: 2000-07-07
PLICATION NUMBER: 60/225,270
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LING DATH: 2000-12-08
PELICATION NUMBER: 60/235,834
LING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: 60/234, 274
LING DATE: 2000-09-21
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LING DATE: 2000-09-21
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:LING DATE: 2000-08-30
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LING DATE: 2000-08-14
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LING DATE: 2000-09-29
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ILING DATE: 2000-09-14
PPLICATION NUMBER: 60/220,964
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APPLICATION NUMBER: 60/229,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/229,343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICATION NUMBER: 60/229,345
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                          PRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-764-903-19
1 Sequence 19, Application US/09764903
2 Fatent No. US20020090674A1
3 FALEN No. US20020090674A1
3 APPLICANT: Rosen et al.
3 TITLE OF INVENTYON: Nucleic Acids, Proteins, and Antibodies
3 TITLE REFERENCE: PT28
3 CURRENT APPLICATION NUMBER: US/09/764,903
3 CURRENT FILING DATE: 2001-01-17
5 Frior application data removed - consult PALM or file wrapper
5 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1998
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                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
PERATURE:
OTHER INFORMATION: protein phosphatase 4 (formerly x),
OTHER INFORMATION: catalytic subunit (PPP4C) gene.
                                                                                                                                                                                                                                                                                                                                              Query Match
1.3%; Score 49; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 49; Conservative 0; Mismatches 0;
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1.3%; Score 49; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.1e-1:
Matches 49; Conservative 0; Mismatches (
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTHARE: Patentin Ver: 2.1
ENGTH: 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/10091391
Publication No. US20030082681A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ ID NO 19
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-903-19
                                                                                                                                                                                                                                                                                                     US-10-007-926A-34
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US-10-091-391-19
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PRIOR PRICK PAPIL CAPITO NUMBERS: 60/236, 367
PRIOR PELING DATE: 2000-10-22
PRIOR PELING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR PELING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-11-03
PRIOR PELING
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PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-16
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PRIOR FILING DATE: 2000-09-14
PRIOR PRIOR PRIOR DATE: 2000-09-14
PRIOR PRIOR DATE: 2000-10-09
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PRIOR PRIOR DATE: 2000-10-09
PRIOR PRIOR PRIOR DATE: 2000-10-09
PRIOR PRIOR PRIOR DATE: 2000-10-09
PRIOR PRIOR DATE: 2000-10-09
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, ORGANISM: Homo sapiens
US-10-436-523-32
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US-10-436-523-33
                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 32
LENGTH: 2713
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                         Gaps
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; Publication No. US20030180888A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TILE REFERENCE: 7853-244-999
; CURRENT APPLICATION UNMER: US/10/436,523
; CURRENT FILING DATE: 2003-12
; PRIOR FILING DATE: 2003-12
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; RIGH APPLICATION NUMBER: 000-111-03
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10436523;
Publication No. US20030180888A1;
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF;
FILE REFERENCE: 7853-244-999;
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT FILING DATE: 2003-11-20;
PRIOR APPLICATION NUMBER: US/10/007,303;
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR APPLICATION NUMBER: 09/706,167
SEQ ID NOS: 100
; SEQ ID NOS: 100
; SEQ ID NO: 1200-11-03
; SEQ ID NO: 1200-11-03
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                                                                                                                                   Query Match
1.3%; Score 49; DB 15; Length 2713;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 49; Conservative 0; Mismatches 0; Indels
                                          Length 2143;
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                                       DB 16; L
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                                       Query Match
1.3%; Score 49; DB
Best Local Similarity .100.0%; Pred. No. 1.1
Matches 49; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 49; Conservative
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CRGANISM: Homo sapiens
US-10-436-523-31
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US-10-436-523-1
US-10-264-049-740
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Sequence 32, Application US/10436523

Sequence 32, Application US/10436523

Rublication No-US2003018088A1

GENERAL INPORMATION:

TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

FILE REPERENCE: 7853-244-999

CURRENT APPLICATION NUMBER: US/10/436,523

PRIOR APPLICATION NUMBER: US/10/007,303

PRIOR PLING DATE: 2001-11-20

PRIOR FILING DATE: 2000-11-03

PRIOR FILING DATE: 2000-11-03

NUMBER OF SEQ ID NOS: 100

SOFFTARRE: Patentin version 3.1
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APPLICANT: FRASE, Christopher C.

FITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

FILE REFERENCE: 7683-244-999

CURRENT APPLICATION NUMBER: US/10/436,523

CURRENT APPLICATION NUMBER: US/10/007,303

PRIOR APPLICATION NUMBER: US/10/007,303

PRIOR PILING DATE: 2001-11-20

PRIOR FILING DATE: 2001-11-03

NUMBER OF SEQ ID NOS: 100

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 33

LENGTH: 2713
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; Sequence 34, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TILE OF INVENTION: CL2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REPERENCE: 7853-244-999
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Pred. No. 1.1e-11;
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Best Local Similarity 100.0%; Pred. No. 1.1.
Best Local Similarity 0; Mismatches
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Sequence 33, Application US/10436523

Publication No. US20030180888A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.3%;
Best Local Similarity 100.0%;
Matches 49; Conservative 0
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TITLE OF INVENTION: Identification of Essential Genes in Aspergillus funigatus and TITLE OF INVENTION: Identification of Essential Genes in Aspergillus funigatus and TITLE OF INVENTION: Methods of Use FILE REFERENCE: 10182-018-999

CURRENT APPLICATION NUMBER: US 60/285,697

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR FILING DATE: 2001-04-27

PRIOR PLILNG DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/295,890

PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR PLILNG DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05
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Merberg, David
Treay, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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COMPUTER: IBM PC_LOS/MS-DOS
COFERATING SYSTEM: PC_LOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: IS-Jun--2000
CLASSIFICATION: CUNKNOWN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.3%; Score 49; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 49; Conservative 0; Mismatches 0;
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A
REGISTRATION NUMBER: 41,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-6558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 6558
LENGTH: 3362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS
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US-09-745-763-20
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## APPLICANT: Ho, Weng;
## APPLICANT: Tishkoff, Daniel
## APPLICANT: Zamudio, Carlos
## APPLICANT: Zamudio, Carlos
## APPLICANT: Lemieux, Sebastien M
## APPLICANT: Lemieux, Sebastien M
## APPLICANT: Lemieux, Sebastien M
## TITLE OF INVENTION: Methods of Use
## TITLE OF INVENTION: Methods of Use
## TITLE OF INVENTION: Methods of Use
## TILE OF INVENTION: Methods of Use
## TILE OF INVENTION: MUMBER: US 60/285,697
## PRIOR APPLICATION NUMBER: US 60/285,697
## PRIOR PAPLICATION NUMBER: US 60/295,890
## PRIOR PELING DATE: 2001-04-27
## PRIOR PELING DATE: 2001-06-05
## PRIOR PELING DATE: 2001-06-05
## PRIOR PELING DATE: 2001-06-05
## PRIOR PELING DATE: 2001-07-09
## PRIOR PELING DATE: 2001-08-31
## NUMBER OF SEQ ID NOS: 8603
## SEQ ID NO 1558
## LEMCH: 2944
## TUDE: NUMBER: LEMCH: LEMC
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1.3%; Score 49; DB 15; I
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 49; Conservative 0; Mismatches 0;
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1.3%; Score 49; DB:
Best Local Similarity 100.0%; Pred. No. 1.14
Matches 49; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION WUMBER: 09/706,167
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
LENGTH: 2713
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US-10-128-714-1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-436-523-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff
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US-10-128-714-6558/c
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US-10-128-714-1558/c
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byat., John C.
APPLICANT: Byat., John C.
APPLICANT: Byat., John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21 (10299)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DATE: 2001-09-24
SEQ ID NOS: 15112
SEQ ID NO 6036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16208, Application US/10085783A
Publication No. US20040037841A1
SERERAL INPORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REPERENCE: 4231/2002
CURRENT APPLICATION UNBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
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OCANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 26-LIB3058-015-Q1-K1-G5
US-09-960-352-6036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.3%; Score 49; DB 15; I
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 49; Conservative 0; Mismatches 0;
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1.3%; Score 48; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 48; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT TILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PELICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-07
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Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-085-783A-16208
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LENGTH: 5362
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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Sincerial Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT FILING DATE: 2002-04-23
FRIOR APPLICANTON NUMBER: US 60/285,697
FRIOR APPLICANTON NUMBER: US 60/285,890
FRIOR APPLICANTON NUMBER: US 60/303,899
FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARR: PARENT: APPLICANTON VURBER: US 60/303,899
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SEQ ID NO 558
LENGTH: 4944
TYDEN NANA
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APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Ensieur, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
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                                                                                                                                                                                                                    1.3%; Score 49; DB 9; Length 4237; Local Similarity 100.0%; Pred. No. 1.1e-11; les 49; Conservative 0; Mismatches 0; Indels
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1.2e-11;
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US-09-745-763-20
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5. US20030119013A1
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US-10-128-714-558
      TYPE: nucleic acid
STRANDEDNESS: double
                                                                    TOPOLOGY: linear
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREENTS: 38-21 (53233) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 54555
LENGTH: 462
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100.0%; Pred. No. 2.9e-11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             Length 372;
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APPLICANT: HYGEG, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REPERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR PILING DATE: 1999-01-20
                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_142572C.1
US-10-424-599-47139
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1.3%; Score 48; DB 13; I
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 48; Conservative 0; Mismatches 0;
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US-10-424-599-54555
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SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 16319
LENGTH: 401
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Sequence 16319, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 48; Conservative
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ORGANISM: Glycine max
                                                                  TYPE: DNA
ORGANISM: Glycine max
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; ORGANISM: Homo !
US-09-918-995-16319
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         SEQ ID NO 47139
LENGTH: 372
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Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Low Young Thus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38 -21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
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FUBLication No. US20040013663A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPERENCE: 4231/202-09-12
TITLE OF INVENTION NUMBER: US/10/242,535A
CURRENT APPLICATION NUMBER: US 10/085,783
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR APPLICATION NUMBER: US 60/275,017
FRIOR APPLICATION NUMBER: US 60/275,017
FRIOR APPLICATION NUMBER: US 60/275,017
FRIOR APPLICATION NUMBER: US 60/271,955
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2.9e-11;
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Pred. No. 2.9e-11;
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1.3%; Score 48; DB
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 48; Conservative 0; Mismatches
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
LENGTH: 348
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US-10-242-535A-16208
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Sequence 95989, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL GENERAL
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1.3%; Score 48; DB 13; L
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 48; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(751)
OTHER INFORMATION: unsure at all n locations
FEATURE:
                                            NAME/KEY: SITE
COCATION: (619)
COCATION: (619)
US-10-351-334-58
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GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Price, Jennifer L.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
OTHER INFORMATION: n equals a,t,g,
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Matthew, Abraham V.
Ledford, Brooke L.
Woesbner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slader, Ted
Davis, Keith R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 34
US-10-424-599-95989
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US-09-770-445-579/c
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APPLICANT:
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                       Query Match 1.3%; Score 48; DB 13; Length 544; Best Local Similarity 100.0%; Pred. No. 3e-11; Matches 48; Conservative 0; Mismatches 0; Indels
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US-10-424-599-46783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58, Application US/10351334 Publication No. US20040034196A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Glycine max
                                                                                                                                          RESULT 32
US-10-424-599-46783/c
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LOCATION: (526)
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Length 1837;

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, ORGANISM: Homo Sapien
US-10-219-535-39
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ITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hurban, Neith
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LABliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 579
LENGTH: 865
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LING DATE: 2002-08-14
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PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR APPLICATION NUMBER: 60/069873
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079286
PRIOR PILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
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No. US20040044179A1
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; ORGANISM: Arabidopsis thaliana
US-09-770-445-579
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-
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APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCEDING THE SAME
FILE REPERENCE: P3530PIC103
CURRENT APPLICATION NUMBER: US/10/232,230
CURRENT FILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062113
PRIOR APPLICATION NUMBER: 60/06349
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
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PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
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PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-27
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                                                         Gaps
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                                                   0; Indels
Ouery Match
1.3%; Score 48; DB 13;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney, Austin L. Smith, Victoria Stephan, Victoria Stephan, Jean-Philippe F. Watanabe, Colin L. Wood, William I.
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US-10-232-224-39
; Sequence 39, Application US/10232224
                                                                                                                                                                                                                                                                                            Application US/10232230 to. US20040044180A1
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Best Local Similarity 100.
Matches 48; Conservative
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
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US-10-232-230-39
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APPLICATION NUMBER: 00/08553
APPLICATION NUMBER: 60/08559
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/08559
FILING DATE: 1998-05-22
FILING DATE: 1998-05-27
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
FILING DATE: 1998-06-17
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090691
APPLICATION NUMBER: 60/090695
APLING DATE: 1998-06-25
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/095318
FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/095916
FILING DATE: 1998-08-14
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FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
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PPLICATION NUMBER: 60/099598
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APPLICATION UNDRER: 60/08441
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/085323
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ING DATE: 1998-07-07
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APPLICATION NUMBER: 60/095302
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ILING DATE: 1998-08-31
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FILING DATE: 1998-09-10
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PPLICATION NUMBER: 60/082804
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                                     CATION NUMBER:
FILE REFERENCE: P3530P1C79
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PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/06419
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PLING DATE: 1999-12-17
PRIOR PLING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: 60/079910
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-27
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                                                                                                                                                                                            APPLICANT: Godowski, Paul J.
APPLICANT: Grainaldi, J. Christopher
APPLICANT: Gurnaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PL0111
CURRENT APPLICATION NUMBER: US/10/232,224
CURRENT APPLICATION NUMBER: US/10/19,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
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Pred. No. 3.2e-11;
); Mismatches 0;
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Grimaldi, J. Christopher
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Publication No. US20030027988A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Partiches 48; Conservative 0;
      Publication No. US20030065147A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker, Kevin P.
Desnoyers, Luc
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin Smith, Victoria
                                                                   : Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trype: DNA CORGANISM: Homo Sapien US-10-232-224-39
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APPLICANT: Baker, Ke
APPLICANT: Desnoyer
APPLICANT: Gerritse
APPLICANT: Goddard,
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US-10-227-884-39
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LENGTH: 1837
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CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1998-03-26
PRIOR PRIOR APPLICATION NUMBER: 60/078910
PRIOR PRIOR DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR PRICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/079728
PRIOR PRILING DATE: 1998-04-26

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PRIOR FILING DATE: 1998-0-10
PRIOR APPLICATION NUMBER: 60/09912
PRIOR APPLICATION NUMBER: 60/10038
PRIOR APPLICATION NUMBER: 60/10038
PRIOR APPLICATION NUMBER: 60/10038
PRIOR APPLICATION NUMBER: 60/10038
PRIOR PLINED DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/10038
PRIOR PLINED DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/10039
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PRIOR APPLICATION NUMBER: 60/10039
PRIOR PLINED DATE: 1998-09-16
PRIOR PLINED DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/10049
PRIOR PLINED DATE: 1998-09-16
PRIOR PLINED DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/10178
PRIOR PLINED DATE: 1998-09-17
PRIOR PLINED DATE: 1998-09-17
PRIOR PLINED DATE: 1998-09-17
PRIOR PLINED DATE: 1998-09-24
PRIOR PLINED DATE: 1998-10-29
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PRIOR PLINED DATE: 1998-10-29
PRIOR PLINED DATE: 1998-10-29
PRIOR PRIOR DATE: 1998-10-29
PRIOR PRIOR DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/10565
PRIOR APPLICATION NUMBER: 60/10565
PRIOR PRIOR DATE: 1998-11-17
PRIOR PLINED DATE: 1998-10-20
PRIOR PRIOR PRIOR DATE: 1998-10-20
PRIOR PRIOR DATE: 1998-10-20
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PRIOR PLINED DATE: 1998-10-20
PRIOR PRIOR DATE: 1999-10-20
PRIOR PLINED DATE: 1999-0-10-20
PRIOR PRIOR DATE: 1999-0-10-20
PRIOR PRIOR DATE: 1999-0-10-20
PRIOR APPLICATION NUMBER: 60/113518
PRIOR PLINED DATE: 1999-0-10-20
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UMBER: 60/062287997-10-17 1997-10-17 1997-10-28 1997-10-28 UMBER: 60/06410. 1997-12-17 1997-12-17 1997-12-17 1998-03-20 UMBER: 60/079291 1998-03-25 UMBER: 60/079291	UMBER: 60 11998-03-2 11998-04-1 11998-04-1 11998-04-1 11998-04-2 11998-05-0 11998-05-0 11998-05-0 11998-05-0 11998-05-0 11998-05-0 11998-05-0 11998-05-0 11998-05-0 11998-05-1 11998-05-1 11998-05-1 11998-05-1 11998-05-1	11998-06-2 TUMBER: 60 11998-06-2 TUMBER: 60 TUMBER: 60 11998-07-0 11998-07-0 11998-08-0 11998-08-0 11998-08-0 TUMBER: 60 11998-08-0	1998-08-31 1998-09-09 1998-09-09 WUMBER: 60/0959 TUPSER: 60/09980 1998-09-10 WUMBER: 60/09981 1998-09-10 WUMBER: 60/09981 1998-09-10 WUMBER: 60/09981 1998-09-10
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PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100390
PRIOR PRINCE DATE: 1998-09-15
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PRIOR PRINCE DATE: 1998-09-15
PRIOR PRINCE DATE: 1998-09-16
PRIOR PRINCE DATE: 1998-09-24
PRIOR PRINCE DATE: 1998-10-20
PRIOR PRINCE DATE: 1999-10-20
PRIOR PRINCE DATE: 1999-10-12
PRIOR PRINCE DATE: 1999-10-12
PRIOR PRINCE DATE: 1999-10-12
PRIOR PRINCE DATE: 1999-10-12
PRIOR PRINCE DATE: 1999-00-12

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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritae, Mary
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Vactoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICATION NUMBER: US/10/218, 631
TITLE OF INVENTION: ADVERSE: 00/06913
FRIOR FILING DATE: 2002-04-09
FRIOR PELING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/06913
FRIOR PELING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/06913
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-10-31
FRIOR APPLICATION NUMBER: 60/06913
FRIOR FILING DATE: 1998-03-20
PRIOR APPLATION NUMBER: ov,
PRIOR PILING DATE: ..
PRIOR PELICATION NUMBER: ov,
PRIOR PELICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
IENGTH: 1837
TURE: DNA
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TOR: DN
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Sequence 39, Application US/10218631
Publication No. US20030045687A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapien
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Lamaldi, Austin. Christopher

Levincant: Smith, Victoria

APPLICANT: Scheban, Jean-Philippe F.
APPLICANT: Scheban, Jean-Philippe F.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wacod, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P35.091C92
CURRENT FILING DATE: 2002-08-28
FRIOR PELING DATE: 1097-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-1
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1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                              PRIOR FILING DATE: 1999-06-22
PRIOR PEDICATION NUMBER: 60/140723
PRIOR PELICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-08-03
PRIOR PELING DATE: 1999-08-03
PRIOR PELING DATE: 1999-08-03
PRIOR PELING DATE: 1999-08-17
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-10-09
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PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
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FILE REFERENCE: P3530P1C1
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; ORGANISM: Hom
US-10-216-159A-39
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APPLICANT: Gerriteen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Gurmaldi, J. Christopher
APPLICANT: Gurmaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, Milliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC98
CURRENT APPLICANTON NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
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PRIOR APPLICATION NUMBER: 06/059113

PRIOR PLING DATE: 2002-04-09

PRIOR PLING DATE: 2002-04-09

PRIOR PLING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/06227

PRIOR APPLICATION NUMBER: 60/06349

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-31

PRIOR PLING DATE: 1998-10-20

PRIOR PLING DATE: 1998-03-25

PRIOR PLING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079294

PRIOR PLING DATE: 1998-03-25

PRIOR PRING DATE: 1998-03-26

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                                                                                                                                                            0; Indels
                                                                              Query Match
1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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1S-10-216-159A-39
Sequence 39, Application US/10216159A
; Publication No. US20030069397A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/10230414 Publication No. US20030050448A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo Sapien
US-10-230-414-39
US-10-218-631-39
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NAPLICANT: BARE, KEVIN P.

APPLICANT: Geddowski, Deficion of the property of t
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APPLICANT: Goddard, Mariy
APPLICANT: Goddard, Maley
APPLICANT: Guth, Victoria
APPLICANT: Guth, Victoria
APPLICANT: Guth, Victoria
APPLICANT: Hand abe, Colin La
APPLICANT: Hood, Milliam I.
TITLE OF INVENTION: SECENTED ENCODING THE SAME
TITLE OF INVENTION WHORER: 10/19, 480
PRIOR APPLICATION NUMBER: 60/063287
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PELING DATE: 1997-09-12-17
PRIOR APPLICATION NUMBER: 60/07928
PRIOR PELING DATE: 1998-00-20
PRIOR PERIOR DATE: 1998-00-20
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1.3%; Score 48; DB 15; Length 18:
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/218,849
CURRENT FILING DATE: 2002-08-12
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/10227873 Publication No. US20030073816A1
                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo Sapien
US-10-218-849-39
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PRIOR APPLICATION NUMBER: 60/08953 PRIOR PLICATION NUMBER: 60/08958 PRIOR PLICATION NUMBER: 60/08905 PRIOR FILING DATE: 1998-06-17 PRIOR PLICATION NUMBER: 60/080905 PRIOR PLING DATE: 1998-06-17 PRIOR PLICATION NUMBER: 60/090472 PRIOR PLING DATE: 1998-06-18 PRIOR PLING DATE: 1998-06-18 PRIOR PLING DATE: 1998-06-25 PRIOR PLING DATE: 1998-06-10 PRIOR PLING DATE: 1998-06-10 PRIOR PLING DATE: 1998-06-10 PRIOR PLING DATE: 1998-06-10 PRIOR PLING DATE: 1998-08-10 PRIOR PLING DATE: 1998-09-10 PRIOR PLING DATE: 1998-09-12 PRIOR PLING DATE: 19
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PRIOR APPLICATION NUMBER: 60/119549
PRIOR PILING DATE: 1999-02-10
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PRIOR PILING DATE: 1999-03-29
PRIOR PILING DATE: 1999-03-29
PRIOR PEDICATION NUMBER: 60/12575
PRIOR PILING DATE: 1999-03-29
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PRIOR PILING DATE: 1999-03-29
PRIOR PILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-05
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PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PELING DATE: 1999-06-23
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-08-3
PRIOR PELING DATE: 1999-11-16
REFIGURE DATE: 1998-11-03
REPLICATION NUMBER: 60/108787
REPLICATION NUMBER: 60/108801
REPLICATION NUMBER: 60/108801
REPLICATION NUMBER: 60/108849
REPLICATION NUMBER: 60/10242
REPLICATION NUMBER: 60/10242
REPLICATION NUMBER: 60/10242
REPLICATION NUMBER: 60/11326
REPLICATION NUMBER: 60/113618
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115565
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APPLICATION NUMBER: 60/115733
FILING DATE: 1999-01-12
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APPLICANT: GodGWER', Paul J.
APPLICANT: GodGWER', Paul J.
APPLICANT: GodGWER', Paul J.
APPLICANT: GodGWER', Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurinely Missin L.
APPLICANT: Gurinely Missin L.
APPLICANT: Gurinely Missin L.
APPLICANT: Waterabe, Colin L.
APPLICANT: Waterabe, Colin L.
APPLICANT: Waterabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: ACIDS ENCORNG THE SAME
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US/10/21/31
PRIOR APPLICATION WHERE: GO/059-113
PRIOR APPLICATION WHERE: GO/069-113
PRIOR APPLICATION WHERE: GO/069-12
PRIOR APPLICATION WHERE: GO/069-13
PRIOR APPLICATION WHERE: GO/069-13
PRIOR APPLICATION WHERE: GO/092-14
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION WHERE: GO/092-15
PRIOR PLING DATE: 1998-03-26
PRIOR PRIOR PLING DATE: 1998-03-26
PRIOR PRIOR PRIOR DATE: 1998-03-15
PRIOR PRIOR PRIOR DATE: 1998-03-15
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1.3%; Score 48; DB 15; 1
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
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, Sequence 39, Application US/10227883
; Publication No. US20030073817A1
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PRIOR PELING DATE: 1998-12-23

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PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/13129

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-13

PRIOR PELING DATE: 1999-

Query Match
1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps

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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Suth, Victoria.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: South, Victoria.
APPLICANT: South, Victoria.
APPLICANT: South, Victoria.
APPLICANT: Wood, Willian L.
APPLICANT: APPLICANTON WOMBER: US/10/219,076
CURRENT APPLICATION WOMBER: US/00/5913
RRIOR APPLICATION WOMBER: 60/06387
RRIOR FILING DATE: 1997-10-31
RRIOR FILING DATE: 1997-10-31
RRIOR FILING DATE: 1997-10-31
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RRIOR FILING DATE: 1998-03-25
RRIOR APPLICANTON WUMBER: 60/063919
RRIOR PRILING DATE: 1998-03-25
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                               Sequence 39, Application US/10219076 Publication No. US20030078379A1 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Iuc
APPLICANT: Gerritesen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
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US-10-219-076-39
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APPLICANT: Grimmaldi, J. Christopher
APPLICANT: Guren, Martin L.
APPLICANT: Graphy, Victoria
APPLICANT: Graphy, Vi
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ACIDS ENCODING NUMBER: US/10/21 NUMBER: US/10/21 NUMBER: 10/119,480 2002-04-09 NUMBER: 60/059113 1997-10-17 1997-10-17 NMBER: 60/063549 1997-10-28 NMBER: 60/06313	NUMBER: 60/069873 NUMBER: 60/078910 NUMBER: 60/079299 NUMBER: 60/079299 1998-03-25 NUMBER: 60/0795680 NUMBER: 60/07928910 1998-03-25 NUMBER: 60/081951 1998-04-15 NUMBER: 60/081951 1998-06-15 NUMBER: 60/08444 NUMBER: 60/08444 NUMBER: 60/08444 NUMBER: 60/08537 1998-05-06 NUMBER: 60/08537 1998-05-13 NUMBER: 60/08537 1998-05-13 NUMBER: 60/08537 1998-05-13 NUMBER: 60/08537 1998-05-13 NUMBER: 60/08537 1998-06-17 NUMBER: 60/08537 1998-06-17 NUMBER: 60/08537 1998-06-17 NUMBER: 60/08537 1998-06-17 NUMBER: 60/08537	NUMBER: 60/090597 1998-06-24 1998-06-25 NUMBER: 60/090695 NUMBER: 60/091982 1998-06-25 NUMBER: 60/091982 1998-07-07 1998-08-04 NUMBER: 60/095318 NUMBER: 60/095318 1998-08-04 NUMBER: 60/095916 1998-08-10 NUMBER: 60/096791 1998-08-11 NUMBER: 60/096791 1998-08-11 NUMBER: 60/096954 1998-08-26 NUMBER: 60/096954 1998-08-26 NUMBER: 60/096959 NUMBER: 60/096959 NUMBER: 60/096959 NUMBER: 60/096959 1998-08-08-11 NUMBER: 60/096959 NUMBER: 60/096959
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PRIOR FILING DATE: 1998-09-10
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PRIOR PRINCHING DATE: 1998-09-17
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PRIOR PRINCH DATE: 1999-10-12
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PRIOR PRINCH

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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabok, Colin L.
APPLICANT: Wood, William L.
APPLICANT: WORBER: US/10/19,464
CURRENT APPLICATION NUMBER: US/10/19,464
PRIOR APPLICATION NUMBER: 60/06213
PRIOR FILING DATE: 1997-09-17
PRIOR PRILNG DATE: 1997-10-29
PRIOR PRILNG DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/06349
PRIOR PRILNG DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/07910
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079966
PRIOR APPLICATION NUMBER: 60/079966
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1.3%; Score 48; DB
Best Local Similarity 100.0%; Pred. No. 3.2
Matches 48; Conservative 0; Mismatches
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PRIOR FILING DATE: 1997-10-17
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PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/079910
PRIOR PELING DATE: 1998-03-20
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US-10-219-464-39
US-10-219-464-39
; Sequence 39, Application US/10219464
; Publication No. US20030088065A1
; GENERAL INFORMATION:
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-075-39
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; Sequence 39, Application No. US20030088064A1
; Sequence 39, Application No. US20030088064A1
; GENERAL INFORMATION:
    APPLICANT: Baker, Kevin F.
    APPLICANT: Geritsen, Mary
    APPLICANT: Goddard, Audrey
    APPLICANT: Goddard, Audrey
    APPLICANT: Grimaldi, J. Christopher
    APPLICANT: Grimaldi, J. Christopher
    APPLICANT: Stephan, Jean-Philippe F.
    APPLICANT: Stephan, Jean-Philippe F.
    APPLICANT: Watanabe, Colin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels C
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CURRENT APPLICATION NUMBER: US/10/219,075
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
                                                                                        PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-05-14
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PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/140723
PRIOR PILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/14073
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-06-26
PRIOR PILING DATE: 1999-06-26
PRIOR PILING DATE: 1999-07-20
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PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
APPLICATION NUMBER: 60/131022
                                                                 LICATION NUMBER: 60/131270
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APPLICANT: Goddwaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PSSOPIC47
CURRENT APPLICATION NUMBER: 105.10/219,466
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                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels (
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1.3%; Score 48; DB 15; L
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1997-12-31
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PRIOR APPLICATION NUMBER: 60/07991
PRIOR APPLICATION NUMBER: 60/07991
PRIOR PELING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-03-27
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SEQ ID NO 39
LENGTH: 1837
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; ORGANISM: Homo Sapien
US-10-219-466-39
                                                                                                                                                      TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-464-39
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APPLICANT: Geritesn, wary
APPLICANT: Gerdard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephen, Jean-Philippe F.
APPLICANT: Stephen, Jean-Philippe F.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FRICA PPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR PLILORION NUMBER: 60/062287
PRIOR PLILORION NUMBER: 60/062287
PRIOR PLILOR DATE: 1997-09-17
PRIOR PLILOR DATE: 1997-10-17
PRIOR PLILOR DATE: 1997-10-17
PRIOR PLILOR DATE: 1997-10-12
PRIOR PLILORION NUMBER: 60/06349
PRIOR PLILORION NUMBER: 60/06349
PRIOR PLILOR DATE: 1997-10-12
PRIOR PLILOR DATE: 1997-10-12
PRIOR PLILOR DATE: 1997-10-12
PRIOR PLILOR DATE: 1998-13-20
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PRIOR PLILORION NUMBER: 60/069903
PRIOR PLILORION NUMBER: 60/069910
PRIOR PLILORION NUMBER: 60/079266
PRIOR PLILORION NUMBER: 60/079266
PRIOR PLILORION NUMBER: 60/079266
PRIOR PLILORION NUMBER: 60/079266
PRIOR PLILOR DATE: 1998-03-26
PRIOR PRIOR PLILOR DATE: 1998-03-26
PRIOR PLILOR DATE: 1998-03-26
PRIOR PRIOR PLILOR DATE: 1998-03-26
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SEQ ID NO 39
LENGTH: 1837
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100.0%; Pred. No. 3.2e-11;
tive 0; Mismatches 0; Indels (
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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US-10-219-481-39
US-10-219-481-39
; Sequence 39, Application US/10219481
; Publication No. US20030088068A1
; GENERAL INFORMATION:
Sequence 39, Application US/10219479
Publication No. US20030088067A1
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; ORGANISM: Homo Sapien
US-10-219-479-39
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Best Local Similarity
Matches 48; Conserv
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Sequence 39, Application US/10232231 Publication No. US20030088071A1 GENERAL INFORMATION:
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US-10-230-260-39
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APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERMER: P3530PLC28
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/062113
PRIOR APPLICATION NUMBER: 60/062113
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-27
PRIOR PELING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1998-03-25
PRIOR PELING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-27
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimel, Austin L.
APPLICANT: Smith, Victoria L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanabe, Colin L.
APPLICANT: Mood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERRNCE: P3530PLG3
CURRENT APPLICATION NUMBER: US/10/2007
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PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-481-39
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GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritaen, Mary
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: P350PL014
FRIOR PILLING DATE: 2002-08-29
FRIOR APPLICANTON NUMBER: 60/66287
FRIOR APPLICANTON NUMBER: 60/66313
FRIOR APPLICANTON NUMBER: 60/66349
FRIOR APPLICANTON NUMBER: 60/66349
FRIOR APPLICANTON NUMBER: 60/66369
FRIOR APPLICANTON NUMBER: 60/66393
FRIOR APPLICANTON NUMBER: 60/06893
FRIOR APPLICANTON NUMBER: 60/06893
FRIOR APPLICANTON NUMBER: 60/06893
FRIOR APPLICANTON NUMBER: 60/078910
FRIOR APPLICANTON NUMBER: 60/078910
FRIOR PILLING DATE: 1998-03-20
FRIOR APPLICANTON NUMBER: 60/078910
FRIOR PILLING DATE: 1998-03-20
PRIOR FILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-28
PRIOR PLILING DATE: 1997-10-28
PRIOR PLILING DATE: 1997-10-31
PRIOR PLILING DATE: 1997-10-31
PRIOR PLILING DATE: 1997-12-17
PRIOR PLILING DATE: 1997-12-17
PRIOR PLILING DATE: 1998-03-20
PRIOR PLILING DATE: 1998-03-20
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PRIOR PLILING DATE: 1998-03-25
PRIOR PLILING DATE: 1998-03-25
PRIOR PLILING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-28
PRIOR PLING DATE: 1998-03-28
PRIOR PLING DATE: 1998-03-3-27
PRIOR PLING DATE
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1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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; Sequence 39, Application US/10218956; Publication No. US20030092887A1; GENERAL INFORMATION:
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul
Grimaldi, J. C
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; ORGANISM: Homo Sapien
US-10-216-165-39
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gramely, Faul J.
APPLICANT: Grimely, Justin L.
APPLICANT: Grimely, Justin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: MATANABE: US/10/232,233
CURRENT FILING DATE: 2002-04-09
FRIOR FILING DATE: 1097-09-17
FRIOR APPLICATION NUMBER: 60/062287
FRIOR PILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/06287
FRIOR PILING DATE: 1997-10-17
FRIOR PILING DATE: 1997-10-17
FRIOR PILING DATE: 1997-10-17
FRIOR PILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/06349
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/06366
FRIOR FILING DATE: 1998-03-25
FRIOR APPLICATION NUMBER: 60/079266
FRIOR APPLICATION NUMBER: 60/079266
FRIOR FILING DATE: 1998-03-25
FRIOR APPLICATION NUMBER: 60/079266
FRIOR FILING DATE: 1998-03-25
FRIOR APPLICATION NUMBER: 60/079266
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
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                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Best Local Similarity 100.0%;
Matches 48; Conservative 0
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CORGANISM: Homo Sapien
US-10-232-233-39
                                                                                                                                TYPE: DNA
CORGANISM: Homo Sapien
US-10-232-231-39
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APPLICANT: Goddweki, Paul J.
APPLICANT: Goddweki, Paul J.
APPLICANT: Gurneld, J. Christopher
APPLICANT: Gurneld, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANTE MATER TORD WATER COLIN COLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR PILING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-15
PRIOR PILING DATE: 1998-09-16
PRIOR PILING DATE: 1998-09-24
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-11-19
PRIOR PILING DATE: 1998-12-23
PRIOR PILING DATE: 1998-12-23
PRIOR PILING DATE: 1998-12-23
PRIOR PILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-13
PRIOR PILING DATE: 1999-13-13

                                       Stephan, Jean-Philippe F. Watanabe, Colin L. Wood, William I.
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APPLICANT: GOGGGACA, AGGGES

APPLICANT: GOGGGACKI, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Surich, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanaba, Colin L.
APPLICANT: Watanaba, Colin L.
APPLICANT: Wood, William L.
APPLICANT: WOOG, William L.
APPLICANT: WOOG, WILLS ENCODING THE SAME
FILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: SCRETED AND THE SAME
FILE OF INVENTION WUMBER: US/10/219, 480
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06313
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-12-17
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SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 48; DB 15; Length 1837;
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          PRIOR PELLING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-17
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PRIOR PELLING DATE: 1997-10-28
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PRIOR PELLING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07954
PRIOR PELING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
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Publication No. US20030092889A1
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Best Local Similarity 100.
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-468-39
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/219,468
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Gerritsen, Mary
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
                                               PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR PILING DATE: 1999-04-26
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PELING DATE: 1999-04-27
PRIOR PELING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1999-06-28
PRIOR PILING DATE: 1999-06-28
PRIOR PILING DATE: 1999-06-22
PRIOR PELING DATE: 1999-06-22
PRIOR PELING DATE: 1999-06-22
PRIOR PELING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-08-03
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
DR FILING DATE: 1999-04-05
DR APPLICATION NUMBER: 60/130232
DR FILING DATE: 1999-04-21
DR APPLICATION NUMBER: 60/131022
DR FILING DATE: 1999-04-26
DR APPLICATION NUMBER: 60/131270
DR APPLICATION NUMBER: 60/131291
DR APPLICATION NUMBER: 60/13145
DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/13145
DR PILING DATE: 1999-04-28
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Gaps

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Pred. No. 3.2e-11;
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Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
Wood, William I.
                                                                                                                                       3715 AATGAAAAAAAAAAAAAAAAAA
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Publication No. US20030096362A1
GENERAL INFORMATION:
                                                   Best Local Similarity 100.0%; P. Matches 48; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-233-205-39
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APPLICANT: Baker, Kevin P.
APPLICANT: Condeact, Audrey
APPLICANT: Coddowski, baul J.
APPLICANT: Gerities, baul J.
APPLICANT: Gerities, baul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE
FILE REFERENCE: P3530PLG7
CURRENT APPLICATION NUMBER: US/10/119, 480
FRIOR FILING DATE: 2002-08-14
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/05913
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-11-31
FRIOR FILING DATE: 1997-11-17
FRIOR APPLICATION NUMBER: 60/06933
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-3-3
FRIOR FILING DATE: 1998-03-3-7
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PRIOR APPLICATION UNBER: 60/079294

PRIOR APPLICATION UNBER: 60/079666

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 39

LENGTH: 1837

TYPE. ....
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
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) TYPE: DNA

) ORGANISM: Homo Sapien

US-10-219-536-39
                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-478-39
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APPLICANT: Wacda, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION ACIDS ENCODING THE SAME
FILE OF INTO THE 1 2002-08-29
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 06/06913
PRIOR APPLICATION NUMBER: 60/06913
PRIOR PILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
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                                                             3762
                                                                                                                           Query Match
1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3:2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels (
Indels
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Publication No. US20030096959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
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TYPE: DNA
ORGANISM: Homo Sapien
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APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Hatanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TILLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PS330PLG45
CURRENT APPLICATION NUMBER: US/10/219,072
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 1997-08-13
PRIOR PLILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/05313
PRIOR FILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
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PPLICANT: Goddowski, Paul J.
PPLICANT: Goddowski, Paul J.
PPLICANT: Grimaldi, J. Christopher
PPLICANT: Gurney, Austin L.
PPLICANT: Smith, Victoria
PPLICANT: Stephan, Jean-Philippe F.
PPLICANT: Watenabe, Colin L.
PPLICANT: Wood, William I.
PPLICANT: Wood, William I.
ITLE OF INVENTION: SCEEETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
LERERENCE: P3530PLCS9
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00.0%; Pred. No. 3.2e-11;
ve. 0; Mismatches 0;
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Best Local Similarity 100.
Matches 48; Conservative
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CORGANISM: Homo Sapien
US-10-219-072-39
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PRIOR FILING DATE: 1997-01-77
PRIOR PLINK DATE: 1997-01-77
PRIOR PLINK DATE: 1997-01-77
PRIOR PLINK DATE: 1997-01-77
PRIOR PLINK DATE: 1997-10-17
PRIOR PLINK DATE: 1997-12-17
PRES. DATE: 199
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William B.
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPRENCE: P3530PIC37
CURRENT APPLICATION NUMBER: US/10/219,524
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR PLILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NOW SEQ ID NOS: 246

LENGTH: 1837

TINE: DNA

ORGANISM: Homo Sapien

US-10-219-474-39
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0, 3.2e-11; Indels
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100.0%; Pred. No. 3.2e-11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 Query Match 1.3%; Score 48; DB Best Local Similarity 100.0%; Pred. No. 3.2 Matches 48; Conservative 0; Mismatches
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PRIOR PELICATION NUMBER: 10/19,480
PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR PILING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-27
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Gerriteen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/10219524 Publication No. US20030096962A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
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; ORGANISM: Homo Sapien
US-10-219-524-39
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Sequence 39, Application US/10219528 Publication No. US20030096963A1 GENERAL INFORMATION:
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R FILING DATE: 1998-09-25

R APPLICATION NUMBER: 60/101916

R APPLICATION NUMBER: 60/101922

R FILING DATE: 1998-09-24

R APPLICATION NUMBER: 60/101922

R APPLICATION NUMBER: 60/106178

R FILING DATE: 1998-10-28

R APPLICATION NUMBER: 60/106484

R APPLICATION NUMBER: 60/106484

R APPLICATION NUMBER: 60/10695

R FILING DATE: 1998-11-30

R FILING DATE: 1998-11-17

R FILING DATE: 1998-11-17

R APPLICATION NUMBER: 60/108961

R FILING DATE: 1998-11-17

R APPLICATION NUMBER: 60/108981

R FILING DATE: 1998-11-17

R APPLICATION NUMBER: 60/108981

R APPLICATION NUMBER: 60/108981

R FILING DATE: 1998-11-17

R APPLICATION NUMBER: 60/108891

R FILING DATE: 1998-11-17

R APPLICATION NUMBER: 60/108891

R FILING DATE: 1998-11-17
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R APPLICATION NUMBER: 60/096791
R APPLICATION NUMBER: 60/097986
R APPLICATION NUMBER: 60/097986
R APPLICATION NUMBER: 60/09654
R APPLICATION NUMBER: 60/099596
R FILING DATE: 1998-08-31
R FILING DATE: 1998-09-09
R FILING DATE: 1998-09-09
R APPLICATION NUMBER: 60/099596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R APPLICATION NUMBER: 60/099803
R FILING DATE: 1998-09-10
R PELLING DATE: 1998-09-10
R PILING DATE: 1998-09-10
R APPLICATION NUMBER: 60/099812
R FILING DATE: 1998-09-10
R APPLICATION NUMBER: 60/099816
R APPLICATION NUMBER: 60/099816
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/095302
R FILING DATE: 1998-08-04
R APPLICATION NUMBER: 60/095318
R FILING DATE: 1998-08-04
R APPLICATION NUMBER: 60/095916
R FILING DATE: 1998-08-10
R APPLICATION NUMBER: 60/096146
R APPLICATION NUMBER: 60/096146
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FILING DATE: 1998-12-15
APPLICATION NUMBER: 60/113296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 1998-09-10
PLICATION NUMBER: 60/100038
LING DATE: 1998-09-11
PLICATION NUMBER: 60/100385
LING DATE: 1998-09-15
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LING DATE: 1998-09-24
PLICATION NUMBER: 60/101741
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PPLICATION NUMBER: 60/101786
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
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Gaps ö Length 1837; Indels Duery Match
1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; PRIOR AFFLICATION NUMBER: 60/11558
PRIOR APPLICATION NUMBER: 60/11558
PRIOR PLING DATE: 1939-01-12
PRIOR APPLICATION NUMBER: 60/123618
PRIOR PLING DATE: 1939-03-19
PRIOR PLING DATE: 1939-03-19
PRIOR PLING DATE: 1939-03-29
PRIOR PLING DATE: 1939-03-29
PRIOR PLING DATE: 1939-04-21
PRIOR APPLICATION NUMBER: 60/13123
PRIOR PLING DATE: 1939-04-2
PRIOR PLING DATE: 1939-04-3
PRIOR PLING DATE: 1939-06-3
PRIOR PLING DATE: 1939-06-3
PRIOR PLING DATE: 1939-06-3
PRIOR PLING DATE: 1939-07-26
PRIOR PLING DATE: 1939-08-17
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PRIOR PRIOR PLING DATE: 1939-08-18
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Sequence 39, Application US/10227880 Publication No. US20030096964A1
   GENERAL INFORMATION:
US-10-227-880-39
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PRIOR PILING DATE: 1998-08-04
PRIOR PILING DATE: 1998-08-07
PRIOR APPLICATION WINDER: 60/09516
PRIOR APPLICATION WINDER: 60/09516
PRIOR APPLICATION WINDER: 60/09514
PRIOR PILING DATE: 1998-08-1
PRIOR PELING DATE: 1998-08-1
PRIOR PILING DATE: 1998-08-1
PRIOR PILING DATE: 1998-08-1
PRIOR PILING DATE: 1998-09-10
PRIOR PELING DATE: 1998-09-11
PRIOR PELING DATE: 1998-09-11
PRIOR PELING DATE: 1998-09-12
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION VUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-31
R APPLICATION NUMBER: 60/119549
R FILING DATE: 1999-02-10
R APPLICATION NUMBER: 60/12518
R FILING DATE: 1999-03-10
R APPLICATION NUMBER: 60/12529
R FILING DATE: 1999-03-19
R FILING DATE: 1999-03-19
R FILING DATE: 1999-03-23
R APPLICATION NUMBER: 60/125775
R RILING DATE: 1999-03-23
R APPLICATION NUMBER: 60/126773
R FILING DATE: 1999-03-29
R FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                                                     NR APPLICATION NUMBER: 60/130232

RETLING DATE: 1999-04-21

RAPPLICATION NUMBER: 60/131022

RETLING DATE: 1999-04-26

RAPPLICATION NUMBER: 60/131270

RAPLICATION NUMBER: 60/131291

RAPLICATION NUMBER: 60/131291

RETLING DATE: 1999-04-27

RAPLICATION NUMBER: 60/131445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R FILING DATE: 1999-04-28

R APPLICATION NUMBER: 60/134287

R FILING DATE: 1999-05-14

R PELING DATE: 1999-06-22

R FILING DATE: 1999-06-22

R APPLICATION NUMBER: 60/140723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
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Publication No. US20030096965A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLING DATE: 1999-07-26
PPLICATION NUMBER: 60/146222
LLING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: 60/141037
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FILING DATE: 1999-07-20
APPLICATION NUMBER: 60/145698
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PILING DATE: 1999-08-03
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##IOR PLILOR NUMBER: 100 19386

##IOR PLILOR DATE: 10986 08 26

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##IOR PARIOR DATE: 10986 09 03

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##IOR PARIOR DATE: 10986 09 013

##IOR PARIOR DATE: 10986 09 014

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PRIOR FILING DATE: 1998-09-09

PRIOR APPLICATION NUMBER: 60/099613

PRIOR PLING DATE: 1998-09-10

PRIOR PLING DATE: 1998-09-15

PRIOR PLING DATE: 1998-09-16

PRIOR PLING DATE: 1998-09-17

PRIOR PLING DATE: 1998-09-24

PRIOR PLING DATE: 1998-09-24

PRIOR PLING DATE: 1998-10-30

PRIOR PLING DATE: 1998-11-17

PRIOR PLING DATE: 1998-11-17

PRIOR PLING DATE: 1998-11-18

PRIOR PLING DATE: 1998-10-30

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PRIOR PRIOR DATE: 1999-10-12

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FILING DATE: 1999-04-05
                                     TITLE OF INVENTION: SCREWED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530PLCH; TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530PLCH; CURENT APPLICATION NUMBER: US/10/227,882 CURRENT FILING DATE: 2002-08-26 PRIOR APPLICATION NUMBER: 10/119,480 PRIOR PILING DATE: 10/02-04-09 PRIOR FILING DATE: 10/02-04-09 PRIOR FILING DATE: 10/02-04-09 PRIOR FILING DATE: 1997-09-17 PRIOR FILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-28 PRIOR PILING DATE: 1997-10-21 PRIOR PILING DATE: 1997-10-21 PRIOR PILING DATE: 1997-12-17 PRIOR PILING DATE: 1998-09-20
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PRIOR PILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-05-06
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PRIOR PILING DATE: 1998-05-13
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PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-06-27
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-08-04
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ILING DATE: 1998-09-09
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APPLICATION NUMBER: 60/079294
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Vaccoria
APPLICANT: Santh, Victoria
APPLICANT: Santh, Victoria
APPLICANT: Santh, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood William I.
APPLICANTON NUMBER: US/10/232,223
CURRENT PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06393
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/06393
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 2002-04-09
PRIOR PLILING DATE: 2002-04-09
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-28
PRIOR PLILING DATE: 1997-10-31
PRIOR PLILING DATE: 1997-12-17
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PRIOR PLILING DATE: 1998-03-28
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1.3%; Score 48; DB 15; 1
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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Publication No. US2030096968A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Genovers, Lack
APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-436-39
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Publication No. US20030096967A1

GENERAL INFORMATION

APPLICANT: Daker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Geritlen, Mary

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Wood, William I.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
                                                     PRIOR FILING DATE: 1999-04-21
PRIOR PELING DATE: 1999-04-21
PRIOR PAPPLICATION NUMBER: 60/131022
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR APPLICATION NUMBER: 60/13445
PRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/14050
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-10-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-12-07
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PRIOR PILING DATE: 1999-12-07
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US-10-232-229-39
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         PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
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                                                                                                                                                               Query Match 1.3%; Score 48; DB 15; Length 1837; Best Local Similarity 100.0%; Pred. No. 3.2e-11; Matches 48; Conservative 0; Mismatches 0; Indels C
                                                                                                                        Length 1837;
                                                                                                                       Query Match
1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                   Sequence 39, Application US/10232225
Publication No. US20030096969A1
GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
PRIOR APPLICATION NUMBER: 60/079656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-232-225-39
                                                                             TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                    US-10-232-223-39
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Gaps

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APPLICANT:

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFREENCE: P330P1C109

CURRENT APPLICATION NUMBER: US/10/232,227

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/053113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063849

PRIOR APPLICATION NUMBER: 60/063849

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/06973

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

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Pred. No. 3.2e-11;
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100.0%; Pred. No. ...
0; Mismatches
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Goddwski, Paul J.
Godowski, Paul J.
Grimal, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Van-Philippe F.
Watanabe, Colin L.
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Publication No. US20030096971A1
GENERAL INFORMATION:
APPLICANT: Beaker, Kevin P.
APPLICANT: Deemoyers, Luc
APPLICANT: Gentiteen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                  Sequence 39, Application US/10232227
Publication No. US20030096970A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 48; Conservative
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US-10-232-227-39
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PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/069873
PRIOR PLING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/079204
PRIOR PLING DATE: 1998-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 39, Application US/10219060 Publication No. US20030100064A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-232-234-39
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APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwekt, Paul J.
APPLICANT: Grimed, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Smith, Victorin L.
APPLICANT: Smith, Victorin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: MATANABER AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330PLGIO ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/22.
       APPLICANT: Godowski, Faul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gotowski, Paul J.
APPLICANT: Stephan, Jaustin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, John J.
APPLICANT: Stephan, John J.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCREED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REPERENCE: P3530PLC105
CURRENT APPLICATION NUMBER: US/10/232,229
CURRENT APPLICATION NUMBER: US/202-08-29
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-21
PRIOR PILING DATE: 1998-10-31
PRIOR PILING DATE: 1998-10-31
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-37
PRIOR PILING DATE: 1998-03-37
PRIOR PILING DATE: 1998-03-37
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
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No. US20030096972A1
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo Sapien
US-10-232-229-39
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Publication No
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victorin L.
APPLICANT: Smith, Victorin L.
APPLICANT: Smith, Victorin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: PS530P1C22
CURRENT APPLICATION NUMBER: US/10/19, 460
PRIOR APPLICATION NUMBER: 60/063113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246 SEQ ID NO 39 LENGTH: 1837
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1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1938-09-24
PRIOR FILING DATE: 1938-09-25
PRIOR FILING DATE: 1938-09-24
PRIOR PRICKATION NUMBER: 60/101916
PRIOR PLING DATE: 1938-09-24
PRIOR PLING DATE: 1938-09-24
PRIOR PLING DATE: 1938-09-24
PRIOR PLING DATE: 1938-10-13
PRIOR FILING DATE: 1938-10-13
PRIOR FILING DATE: 1938-10-28
PRIOR PLING DATE: 1938-10-29
PRIOR PLING DATE: 1938-11-10
PRIOR PLING DATE: 1938-11-17
PRIOR PLING DATE: 1938-11-13
PRIOR PLING DATE: 1939-11-17
PRIOR PLING DATE: 1939-11-17
PRIOR PLING DATE: 1939-11-17
PRIOR PLING DATE: 1939-11-13
PRIOR PLING DATE: 1939-12-27
PRIOR PLING DATE: 1939-01-12
PRIOR

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APPLICANT: Godowski, Paul B.

APPLICANT: Godowski, Paul B.

APPLICANT: Godowski, Paul B.

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

TITLE OF INVENTION: SECRETED AND TRANSEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSEMBRANE POLYPEPTIDES AND NUCLEIC

CURRENT APPLICATION NUMBER: 60/062103

PRIOR FILING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06349

PRIOR APPLICATION NUMBER: 60/06391

PRIOR APPLICATION NUMBER: 60/079294

PRIOR APPLICATION NUMBER: 60/079294

PRIOR APPLICATION NUMBER: 60/079266

PRIOR APPLICATION NUMBER: 60/079266

PRIOR APPLICATION NUMBER: 60/079266

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritleen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Goddard, Audrey
APPLICANT: Grimald, J. Christopher
APPLICANT: Suthh, Victoria
APPLICANT: Sathh, Victoria
APPLICANT: Sathh, Victoria
APPLICANT: Sathh, Victoria
APPLICANT: Sathh, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Wacanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330PLGS
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330PLGS
CURRENT APPLICATION NUMBER: US/10/216,164
CURRENT PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-04-09
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels (
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; ORGANISM: Homo Sapien
US-10-216-162-39
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APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimey, Austin L.
APPLICANT: Simple, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Maranabe, Colin L.
APPLICANT: Mood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/216,160
CURRENT FILING DATE: 2002-08-09
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NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%; Score 48; DB 15; I Best Local Similarity 100.0%; Pred. No. 3.2e-11; Matches 48; Conservative 0; Mismatches 0;
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                              PRIOR APPLICATION NUMBER: 60/14930
PRIOR PILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR PELING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-13-18
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: 60/16945
PRIOR APPLICATION NUMBER: 60/16945
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
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Publication No. US20030100709A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 48; Conservative
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; ORGANISM: Homo Sapien
US-10-216-160-39
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Gaps

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GREAKAL INCRAMILOR.

APPLICANT: Baker, Kevin P.

APPLICANT: Benery Kevin P.

APPLICANT: Geddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Granaba, Colinita II.

APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Stephan. Jean-Philippe F.
APPLICANT: Watanabe, Colin II.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
THE REPRENCE: P3530PLIO

CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: 60/06389
PRIOR PILING DATE: 1997-03-20
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR PRIOR FILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
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1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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Conservative 0;
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CORGANISM: Homo Sapien
US-10-216-168-39
                                                                                                                                                                                                       LENGTH: 1837
TYPE: DNA
CRGANISM: Homo Sapien
US-10-216-167-39
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Best Local Similarity
Matches 48; Conserv
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APPLICANT: Baker, Kevin P.

APPLICANT: Deenoyers, Luc

APPLICANT: Gedriteen, Mary

APPLICANT: Goddard, Paul J.

APPLICANT: Goddard, Paul J.

APPLICANT: Goddard, Paul J.

APPLICANT: Goddard, Paul J.

APPLICANT: Grimald, J. Christopher

APPLICANT: Grimald, J. Christopher

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Sephan, Jean-Philippe F.

APPLICANT: Wood, William I.

PRIOR FILING DATE: 1997-10-13

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/063873

PRIOR PILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/063873

PRIOR APPLICATION NUMBER: 60/063873

PRIOR PILING DATE: 1997-12-17

PRIOR PILING DATE: 1997-12-17

PRIOR PLING DATE: 1997-12-17

PRIOR PILING DATE: 1997-12-17

PRIOR PILING DATE: 1997-12-17
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SEQ ID NO 39
LENGTH: 1837
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels (
                                                                                      PRIOR APPLICATION NUMBER: 60/06328)
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-18
PRIOR PLING DATE: 1997-10-18
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR PRIOR DATE: 1998-03-26
PRIOR PRIOR DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PRIUG DATE: 1998-03-26
PRIOR PRIUG DATE: 1998-03-26
PRIOR PRIUG DATE: 1998-03-26
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   APPLICATION NUMBER: 60/059113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo Sapien
US-10-216-164-39.
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APPLICANT: STEPhAT, Jean-Philippe F.
APPLICANT: Stephat, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENT SPAPLICATION NUMBER: US/10/219,071
CURRENT APPLICATION NUMBER: US/119,480
PRIOR APPLICATION NUMBER: US/10/39
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-00-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-11-2-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
PRIOR PRILING DATE: 1998-03-26
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APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC IIILE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246 SEQ ID NO 39 SEQ ID NO 39 LENGTH: 1837
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels 0
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CURRENT APPLICATION NUMBER: US/10/219,074
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
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Garritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NT FILING DATE: 2002-08-13
APPLICATION NUMBER: 10/119,480
FILING DATE: 2002-04-09
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Publication No. US20030100715A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-071-39
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APPLICANT: Baker, Mary
APPLICANT: Banoyers, Luc
APPLICANT: Gedard, Audrey
APPLICANT: Gedowski, Paul J.
APPLICANT: Gedowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICANTON: GOIN L.
TITLE OF INVENTION: SCRETED ENCODING THE SAME
FILE REFERENCE: P3530PL039
CURRENT APPLICANTON NUMBER: US/10/219,065
CURRENT APPLICANTON NUMBER: 60/05913
PRIOR FILING DATE: 1097-40-9
PRIOR FILING DATE: 1097-40-9
PRIOR FILING DATE: 1097-10-13
PRIOR FILING DATE: 1097-110-13
PRIOR FILING DATE: 1099-110-13
PRIOR FILING DATE: 1099-10-21
PRIOR PRILICATION NUMBER: 60/06993
PRIOR FILING DATE: 1099-10-29
PRIOR FILING DATE: 1099-03-26
PRIOR PRILICATION NUMBER: 60/079-26
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SEQ ID NO 39
LENGTH: 1837
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1.3%; Score 48; DB 15; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                Sequence 39, Application US/10219065 Publication No. US20030100713A1
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Publication No. US20030100714A1
GENERAL INFORMATION:
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; ORGANISM: Homo Sapien
US-10-219-065-39
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US-10-219-071-39
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Gaps

Gaps

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APPLICANT: BAREAY KAYIN F.
APPLICANT: BAREAY KAYIN F.
APPLICANT: Gartieen, Mary
APPLICANT: Gadowski, Paul J.
APPLICANT: Gadowski, Paul J.
APPLICANT: Gadowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, Milliam I.
APPLICANT: MONBER: 109/10/219,465
CURRENT FILLING DATE: 2002-04-09
FRIOR PELING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/05349
FRIOR APPLICATION NUMBER: 60/063849
FRIOR PILLING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/063849
FRIOR FILING DATE: 1997-10-21
FRIOR PLING DATE: 1997-10-21
FRIOR APPLICATION NUMBER: 60/063849
FRIOR FILING DATE: 1997-10-31
FRIOR APPLICATION NUMBER: 60/063849
FRIOR FILING DATE: 1997-10-31
FRIOR APPLICATION NUMBER: 60/079294
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-22
FRIOR APPLICATION NUMBER: 60/079284
FRIOR FILING DATE: 1998-03-22
                           Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
TYPE: DM
CRGANISM: Homo Sapien
US-10-219-077-39
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                                                                                                                                                                                                                                                                              Query Match 1.3%; Score 48; DB 15; Length 1837; Best Local Similarity 100.0%; Pred. No. 3.2e-11; Matches 48; Conservative 0; Mismatches 0; Indels C
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Publication No. US20030100717A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-465-39
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LENGTH: 1837
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APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC53
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062397
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-10-31
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                                                                       PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-12-17

PRIOR PILING DATE: 1997-12-17

PRIOR PILING DATE: 1997-12-17

PRIOR PILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-25

PRIOR PPLICATION NUMBER: 60/079294

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 39

LENGTH: 1837

TYPE: DNA

ORGANISM: Homo Sapien

US-10-219-074-39
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1.3%; Score 48; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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998-03-25
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APPLICATION NUMBER: 60/079728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/10219077
Publication No. US20030100716A1
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                                                            CATION NUMBER: 60/063549
60/062287
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Gaps

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: MATANABE IN ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLG9
CURRENT FILING DATE: 2002-08-14
CURRENT APPLICATION NUMBER: US/10/119,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR PLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
                APPLICANT: STEPAL, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFREENCES: 23020F165.
CURRENT APPLICATION NUMBER: U0/119,480
PRIOR APPLICATION NUMBER: U0/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
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NUMBER OF SEQ ID NOS: 246
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tive 0; Mismatches
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Publication No. US20030100720A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 48; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo Sapien
US-10-219-469-39
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APPLICANT: Wacanabe, Count.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: PASSOPICAGE

CURRENT PILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR APPLICATION NUMBER: 60/659113

PRIOR APPLICATION NUMBER: 60/659113

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/66287

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-27
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SEQ ID NO 39
LENGTH: 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephan, Jean-Philippe F. Watanabe, Colin L. Wood, William I.
                                                                                                                    US-10-219-467-39
; Sequence 39, Application US/10219467
; Belblication No. US20030100718A1
; GENERAL INFORMATION:
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To. US20030100719A1
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APPLICANT: Baker, Kevin P.
APPLICANT: Describen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Goddowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gurney, Austin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-467-39
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0; Mismatches
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Best Local Similarity 100.
Matches 48; Conservative
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Best Local Similarity 100.
Matches 48; Conservative
NUMBER OF SEQ ID NOS: 246
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US-10-219-476-39
                                                                                                               TYPE: DNA
CRGANISM: Homo Sapien
US-10-219-473-39
                                 SEQ ID NO 39
LENGTH: 1837
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Saith, Victoria
APPLICANT: Saith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: WOOd, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3530PLG35
CURRENT APPLICATION NUMBER: U5/10/219,473
CURRENT PILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-13
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
                                                         PRIOR PELICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
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Pred. No. 3.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0, Mismatches
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Publication No. US20030100721A1
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DATE: 1998-03-27
                                         LING DATE: 1997-10-28
PLICATION NUMBER: 60/064103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 48; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Baker, Kevin P.
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CORGANISM: Homo Sapien
US-10-219-471-39
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APPLICANT: SENEDA, VICTORIA
APPLICANT: SCHEDA, VICTORIA
APPLICANT: STATEN, VICTORIA
APPLICANT: Wetanabe, Colin L.
APPLICANT: Wetanabe, Colin L.
APPLICANT: Worden C.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC36
CURRENT APPLICATION NUMBER: US/10/219,476
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DA
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100.0%; Pred. No. 3.2e-11;
tive 0; Mismatches 0; Indels (
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APPLICANT: Grimali, victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/65287
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/66287
PRIOR FILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/69873
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079266
PRIOR APPLICATION NUMBER: 60/079266
PRIOR APPLICATION NUMBER: 60/07928
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILICATION NUMBER: 60/07928
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-28
PRIOR PI
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100.0%; Pred. No. 3.2e-11;
tive 0; Mismatches 0; Indels (
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Sequence 39, Application US/10227874

Publication No. US2003100724A1

GENERAL INPORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Genencyers, Luc

APPLICANT: Gedard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Guinaldi, J. Christopher

APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephan, Jean-Philippe F.
                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, J. Christopher
                                              Sequence 39, Application US/10219482 Publication No. US20030100723A1 GENERAL INFORMATION:
                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 48; Conserv
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A PELLING DATE: 1998-09-10
R APPLICATION NUMBER: 60/099816
R FILING DATE: 1998-09-10
R APPLICATION NUMBER: 60/10038
R PILING DATE: 1998-09-11
OR APPLICATION NUMBER: 60/100385
                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR PILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100419
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR PILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/10174
PRIOR PILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/10176
PRIOR PILING DATE: 1998-09-24
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PRIOR APPLICATION NUMBER: 60/101916

PRIOR APPLICATION NUMBER: 60/101916

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1998-10-29

PRIOR FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: 60/106464

PRIOR PILING DATE: 1998-10-29

PRIOR PILING DATE: 1998-10-30

PRIOR PILING DATE: 1998-10-30

PRIOR PILING DATE: 1998-11-03

PRIOR PILING DATE: 1998-11-03

PRIOR PILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: 60/10849

PRIOR PILING DATE: 1998-11-17

PRIOR PILING DATE: 1998-11-17

PRIOR PILING DATE: 1998-11-18

PRIOR PILING DATE: 1998-11-18

PRIOR PILING DATE: 1998-11-18

PRIOR PILING DATE: 1998-12-15

PRIOR PILING DATE: 1998-12-15

PRIOR PILING DATE: 1998-12-15

PRIOR PILING DATE: 1998-12-15

PRIOR PILING DATE: 1998-12-22

PRIOR PILING DATE: 1998-12-23

PRIOR PILING DATE: 1998-12-23
PLICATION NUMBER: 60/099811
ILING DATE: 1998-09-10
FILING DATE: 1998-09-10
PPLICATION NUMBER: 60/099812
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APPLICATION NUMBER: 60/115733
FILING DATE: 1999-01-12
FILING DATE: 1999-02-10
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PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
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MBER: 60/125775
.999-03-23
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Sequence 39, Application US/10227876

| Sequence 39, Application US/10227876
| Publication No. US20030100725A1
| GENERAL INPORMATION:
| APPLICANT: Baker, Kevin P. |
| APPLICANT: Gerritsen, Mary | APPLICANT: Goddard, Audrey | APPLICANT: Goddwski, Paul J. |
| APPLICANT: Grimaldi, J. Christopher | APPLICANT: Grimaldi, J. Christopher | APPLICANT: Stephan, Jean-Philippe F. | APPLICANT: Stephan, Jean-Philippe F. | APPLICANT: Wacanabe, Colin L. | APPLICANT: Wood, William I. | IIILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FITTE OF INVENTION: ACIDS ENCODING THE SAME | IIILE OF INVENTION: ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1.3%; Score 48; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 48; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/227,876
CURRENT FILING DATE: 2002-08-26
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/13022
PRIOR PILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-26
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PRIOR PLING DATE: 1999-07-26
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P53.091C76
FURB REPRESENCE: P53.091C76
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
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Matches 48; Conservative 0; Mismatches 0;
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R FILING DATE: 1999-07-28

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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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o. US20030100726A1
CATION NUMBER: 60/131445
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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FILING DATE: 1998-09-10

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ALIGNMENTS

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ABN81319 standard; cDNA; 3762 BP ABN81319;

Human mast cell related gene MC1 SEQ ID NO 1.

Human, mast cell; MC; antiallergic; antiinflammatory; antiasthmatic; vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma; gene; ss.

The invention relates to isolated nucleic acid (ABN81319-ABN81324),

Corresponding to genes differentially expressed in mast cells following
activation or in patients with allergic hypersensitivity disease. [I]
that encodes proteins (ABB77559-ABB77515) [II] or a protein fragment of
that encodes proteins (ABB77559-ABB77515) [II] or a protein fragment of
CC (II) if at least 6 amino acids. (II) is useful for identifying binding
CC partners. (I) or (II) is useful for diagnosing or treating a disease
state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,
cuticaria or atopic dermatitis or mastocytosis) in a subject which
involves determining the level of expression of (I) or (II). A computer
system, comprising a database containing information identifying the
expression level in a tissue or at least one mast cell of (I), is useful
cc for presenting information to identify the relative expression level of
for presenting information to identify the relative expression level of
cc for presenting information con activity and as an antigen to raise
polyclonal or monoclonal antibodies. (II) is useful for identifying
agonts that modulate expression of the protein or agents, such as
agonists or antagonists. The agonists or antagonists are useful for
modulating biological activity and function of (II) and thus are useful
cor alleviating disease conditions such as allergic hypersensitivity,
condulating thinitis, asthma, urticaria, atopic dermatitis or mastocytosis Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity. GAGAAACCGAGTCACTGTGAAAAGATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTG GAGAAACCGAGTCACTGTGAAAAGATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTG 61 GGAGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCCAGATGAGGAAAAGAAAAGCGCAGGAA ACTICIAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATT 121 ATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCC 0; Gaps Query Match 100.0%; Score 3762; DB 6; Length 3762; Best Local Similarity 100.0%; Pred. No. 0; Matches 3762; Conservative 0; Mismatches 0; Indels 0; Sequence 3762 BP; 1220 A; 672 C; 680 G; 1190 T; 0 U; 0 Other; Claim 1; Page 95-97; 119pp; English. Einstein 08-DEC-2000; 2000US-0251835P. 14-MAR-2001; 2001US-0275479P. 28-MAR-2001; 2001US-0259115P. 02-APR-2001; 2001US-0260143P. 07-DEC-2001; 2001WO-US046180 Nocka K, Pirozzi G, WPI; 2002-508560/54. P-PSDB; ABB77569. (UNIO) UCB SA. 13-JUN-2002. -61 181 8 ·S ठ 원 ò 셤 8

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                Crgarddararcrarriraagririrgacarrargaaraaagreecraraaarcaa 3720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                      CTTTTAGTCATTATAATATTTTTTGAGATTCATCTATGTTTAATGTTCTATCAGTAGTTGT
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Pred. No. 3.5e-244;
0; Mismatches 4;
                                                                                                    Human prostate expression marker cDNA 26121
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25-WAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-021314P.
18-UUL-2000; 2000US-0259007P.
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                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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gene; ss.
                    AGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAACTTGTGCTTATA
AGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAACTTGTGCTTATA
                                                                TITIGITIGCAACACACTAGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGGTGGA
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pharmacogenomic marker;
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25-MAY-2000; 2
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                                                                                                                                                                                     GCCAGTGATCCGAGTACTTTGGGAAGCCAAGACAGGTGGATCTCTTGAGCCCCAGGAGTTT
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the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                 TITIGITIGCAACACACTAGITAATITIAACCIGIGACTAGITAICICIACCGAAGGIGGA
                                                                                                                                                                                                                                                                       1853 IGTGTAGTTTCTGGTTTTTAAATTCAAGCAAACTGGAAAATAATCCATCTAATTATGCTT
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                                                                                                                                                                                                                                                                       Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene; ss.
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19.5%; Score 733; DB 5; Length 1128;
Best Local Similarity 99.6%; Pred, No. 3.5e-244;
Matches 933; Conservative 0; Mismatches 4; Indels (
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     2393 GAGGCCAGACTGCACACACAGTGAGACCTCGTTTCT
                              958 GAGGCCAGACTGCACAACACAGTGAGACCTCGTTTCT
                                                                                                                                                                                                                                       Human prostate expression marker cDNA 20797
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0201454P.
19-UUN-2000; 2000US-0211314P.
13-DEC-2000; 2000US-0219007P.
                                                                                                                              ABV20806 standard; cDNA; 1128
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Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene; ss.
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                                                                               538 ATTGACAATGCATTCATTATATATTTTTTTTATAGTTACAGTATACGAGTTGAGTATCC
                                                                                                                                         GAATATITCCATACATATAATGAGAGTTGGAAAAATGGGATTCAAGTCTAATCATAAAA
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                              ATTGACAATGCATTCATTATATATTTT
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25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-021114P.
18-UUL-2000; 2000US-0219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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Best Local Similarity 99.6%; Pred. No. 3.5e-244;
Matches 933; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3347; 11750pp; English.
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                                                                                                           2000US-0183319P.
2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                               25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                       20-FEB-2001;
                                                                                                           17-FEB-2000;
16-MAR-2000;
23-AUG-2001
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether profitestion of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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       838 GTCACTATTTCAAGTCAGTGCTCAAAAAGTTTCAGATGTTAAGCTGGTGATGCTCAT
                                                                                      898 GCCAGTGATCCCAGTACTTTGGGAAGCCAAGACAGGTGGATCTCTTGAGCCCAGGAGTTT
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Best Local Similarity 99.6%; Pred. No. 3.5e-244;
Matches 933; Conservative 0; Mismatches 4; Indels
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                                                                                                                                             2393 GAGGCCAGACTGCACACACAGTGAGACCTCGTTTCT 2429
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25-MAY-2000; 2000US-0207454P.
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18-UUL-2000; 2000US-021017P.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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CDNA sequence, SEQ ID NO:842
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                                                                        Human novel
                ADC30760
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RESULT 10
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ID ADC3
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DT 18-D
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Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; meuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 1; gene; ss.

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WO2003029271-A2

10-APR-2003

24-SEP-2002; 2002WO-US030474.

24-SEP-2001; 2001US-0324631P.

HYSE-) HYSEQ INC

Weng G; Wang J, Wang Z, I Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Haley-Vicente D, Drmanac RT;

WPI; 2003-371981/35. P-PSDB; ADC31731.

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Claim 1; SEQ ID NO 842; 1185pp; English.

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC31889) and the polypeptides they encode (ADC31860-ADC31860). The the invention also relates to nucleic acid sequences over 99\$ identical with the novel human cDNAs in invention and included the invention; the the novel human production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and method of detecting polymolectides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention inthe defection invention in the invention in the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the polymolectide and/or polypeptides of the invention and 767 contig sequences corresponding to the cDNA sequences of the invention and 167 contig sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forcensics, gene mapping, in the identification of mutations responsible for genetic disorders or other trasting diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, andemias, platelet correct also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, andemias, platelet correct of primers, wounds, burns, ulcers, osteoporcosis, autoimmune diseases or care also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically contact this patent did not form part of the printed specification, but was for the printed sequence of the invention. Note: The sequence of the invention of cohemined in electronic formate diseases.

Sequence 667 BP; 216 A; 147 C; 154 G; 150 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences.

Gaps ö 13.5%; Score 506; DB 9; Length 667; 100.0%; Pred. No. 1.4e-165; ive 0; Mismatches 0; Indels Conservative Best Local Similarity Matches 506; Conserv Query Match

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastesized in a patient; determining whether prostate cancer has metastesized in a patient; (l) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; carcinogen; pharmacodyanamic marker;
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for detecting presence of prostate cancer, stage of prostate cancer
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Pred. No. 1.8e-109;
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                                                                                       Page 1680; 11750pp; English.
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pharmacogenomic marker;
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gene; ss.
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                                                                                                                                                                                                                                                                                                                        ATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAAGCCAAGAAGAAGTTTCATCC
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25-MAY-2000; 2000US-0207454P.
09-UTM-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0211314P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient.
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                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACTGGATATTTTTCCATATAACTTGCAGTAATAGTTCAAAAATTAATAGTTTTTGAC
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99.7%; Pred. No. 1.7e-109;
tive 0; Mismatches 1;
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                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                            Monahan JE
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          17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-0211314P.
18-ULL-2000; 2000US-021907P.
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Best Local Similarity 99.7
Matches 394; Conservative
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                                          cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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Human prostate expression marker cDNA 31600.
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2000US-0189862P.
2000US-0207454P.
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2000US-0219007P.
2000US-025281P.
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                                                         Human; prostate cancer;
pharmacogenomic marker;
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Matches 392; Conserv
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16-MAR-2000; 2
25-MAY-2000; 2
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18-JUL-2000; 2
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1635 ATTGGCTTTTCTGAGAAGAGAAATTGAAAGTGTCACAAAATAAAAAAAGATGAAATGAAG

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                    345 TICAAGCAAACIGGAAATAATCCAICTAATTAIGCITTCCTTCCCAAGAAGTTTTTAA 404
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ABV40245
ID ABV40245
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AC ABV40245;
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AC ABV40245;
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I 16-SEP-2002 (first entry)
XX
Human prostate expression marker cl
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Human; prostate cancer; cytostatic
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Human; prostate cancer; cytostatic
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AC ABV2-200; 2000US-0183119P.
PR 23-AUG-2001.
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XX
Z3-AUG-2001.
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Z0-FEB-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0183119P.
PR 25-MAY-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0183119P.
PR 16-MAR-2000; 2000US-0183119P.
PR 18-UUL-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 25-MAY-2000; 2000US-021114P.
PR 25-MAY-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 25-MAY-2000; 2000US-021114P.
PR 25-MAY-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 19-UUL-2000; 2000US-021114P.
PR 25-MAY-2000; 2000US-0211114P.
PR 25-MAY-2000; 2000US-02011114P.
PR 25-MAY-2000; 2000US-0201114P.
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pharmacogenomic marker, gene, ss.
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                                                                                                                                              1815 AATTTAACCTGTGACTAGTTATCTCTACCGAAGGTGGATGTGTAGTTTCTGGTTTTAAAA
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CATATATATTGTCAATTTTTCAATTTTCTAGTCAACAGAGAATCGAAGGATTCTGTTC
                                                          165 CATATATATICICAATITITCAATITICIAGCCAACAGAGAATCGAAGGATICIGTIC
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
9-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0219007P.
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(f) assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastastast in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patie; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                            Sequence 437 BP; 150 A; 63 C; 79 G; 145 T; 0 U; 0 Other;
                                                              Query Match
9.1%; Score 342; DB 5; I
Best Local Similarity 99.7%; Pred. No. 8.6e-109;
Matches 392; Conservative 0; Mismatches 1;
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25 - MAX. 2000; 2000US-0207444P.
09-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-0259007P.
13-DEC-2000; 2000US-0255281P.
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                                prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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Novel isolated nucleic acid molecule associated with cancerous prostate cells and correlating with presence of prostate cancer
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Pred. No. 7e-75;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 446 BP; 146 A; 68 C; 77 G; 152 T; 0 U; 3 Other;
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                                                                                                                                       Claim 1; Page 246; 11750pp; English.
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Matches 344, Conservative
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TATTTTGTTTGCAACACACTAGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGGTG 1850
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                                                        Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker;
pharmacogenomic marker, gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 213; DB 5; Length 421;
Pred. No. 3.8e-64;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 421 BP; 143 A; 61 C; 71 G; 145 T; 0 U; 1 Other;
                   Human prostate expression marker cDNA 31267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 6740; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE
                                                                                                                                                                                                                                                                                                      16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
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Best Local Similarity 99.2%;
Matches 363; Conservative (
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indoblence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 404 BP; 142 A; 54 C; 63 G; 144 T; 0 U; 1 Other;
                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1617-1618; 11750pp; English
                                                                                                                                                              Monahan JE;
                                  09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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215 TATATTTTGTTTGCAACACCACTAGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGG 274

275 TGGATGTGTAGTTTCTGGTTTTAAAATTCAAGCAAACTGGAAAATAATCCATCTAATTAT 334

1909 GCTTTCTTTCCCAAGAAGTTTTTT 1932

1849 IGGAIGIGIAGITITCIGGITITIAAAAITCAAGCAAACIGGAAAATAAICCAICIAAITAI

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100.0%; Pred. No. 5.1e-61;
                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 9584.
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                                                                                                                                                                ABV09593 standard; cDNA; 359 BP
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
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                                                TAATTG 1976
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                                                                               TAATTG 421
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18-JUL-2000;
13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                              Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker,
pharmacogenomic marker, gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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5.4%; Score 203; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 203; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                              Human prostate expression marker cDNA 415.
335 GCTTTCTTTCCCAAGAAGTTTTTT 358
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25-MAY-2000; 2000US-0207454P.
09-UTN-2000; 2000US-021314P.
18-UTL-2000; 2000US-0259007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                       ABV00424 standard; cDNA; 400
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1729 CAACAGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAGAAACTTGTGCT 155 CAACAGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAAACTTGTGCT

1848 214

1789 TATATTTGTTTGCAACACACTAGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGG

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Best Local Similarity 100. Matches 204; Conservative

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1729 CAACAGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAACTTGTGCT

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1789 TATATTTTGTTTGCAACACACACTGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGG
                                                                    258 TATATITITGTITGCAACACACTAGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGG
                                                                                                                                                1849 TGGATGTGTGTTTCTGGTTTTTAAAATTCAAGCAAACTGGAAAATAATCCATCTAATTAT
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                                                                                                                                                                                                                                                                                            GCTTTCTTTCCCAAGAAGTTTTT 1931
                                                                                                                                                                                                                                                                                                                                            378 GCTTTCTTTCCCAAGAAGTTTTT 400
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-02191454P.
09-UUN-2000; 2000US-021314F.
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                                                                                                                 TGGATGTGTAGTTTCTGGTTTTAAAATTCAAGCAAACTGGAAAATAATCCATCTAATTAT 1908
                                                                               318
                                                                                                                                      319 IGGATGTGTGTTTTTTTTTTTTAAATTCAAGCAAACTGGAAAATAATCCATCTAATTAT 378
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199 CAACAGAGAATGGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAAACTTGTGCT
                                                                             259 mararrrrighrracaacacacharraarrraaccrereacraerrarcraccaage
                                               TATATTTTGTTTGCAACACACTAGTTAATTTAACCTGTGACTAGTTATCTCTACCGAAGG
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                                                                                                                                                                                         GCTTTCTTTCCCAAGAAGTTTTT 1931
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25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
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Length 401;

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Query Match 5.45 Best Local Similarity 100.0 Matches 203; Conservative

Sequence 401 BP; 136 A; 58 C; 73 G; 134 T; 0 U; 0 Other;

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                                                 1729 CAACAGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAACTTGTGCT
                                                                                                                                                 259 TATATTTTGTTTGCAACACTAGTTAATTTAACCTGTGACTAGTTATCTCTACGAAGG
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                                                                              199 CAACAGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAACTTGTGCT
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                 0; Mismatches
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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100.0%;
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                 Matches 203; Conservative
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Best Local Similarity
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                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
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                                                                                                                                      1849 IGGAIGIGIAGITICIGGITITAAAATICAAGCAAACIGGAAAATAAICCAICTAATTAI
1729 CAACAGAGAATCGAAGGATTCTGTTCAAATATTAGTAAAAATTGAAAATAAAACTTGTGCT
                                 199 CAACAGAGATCGAAGGATTCTGTTCAATATTAGTAAAAATTGAAAATAAACTTGTGCT
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2000US-0211314P.
2000US-0219007P.
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2000US-0189862P.
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16-MAR-2000;
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Length 337;

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                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I), comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogent potential of a compound; (g) determining whether prostate cancer cancer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient (h)
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assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                       214 TAAAAATTGAAAATAAACTTGTGCTTATATTTTGCTTTGCAACACACTAGTTAATTTAACC
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                                                                                 Length 296;
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                                                                                                                 Indels
                                              Sequence 296 BP; 108 A; 41 C; 50 G; 97 T; 0 U; 0 Other;
                                                                               1.6%; Score 62; DB 5; L
100.0%; Pred. No. 7.3e-12;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate expression marker cDNA 638
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2000US-0207454P.
2000US-0211314P.
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                                                                                                                   Conservative
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                                                                                                 Similarity
                                                                                                                                                                                                                     1824 TG 1825
                                                                                                                                                                                                                                                     TG 275
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25-MAY-2000;
09-JUN-2000;
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                                                                                                                   62;
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                                                                                 Query Match
                                                                                                     Local
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Matches
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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Local Similarity 100.0%; Pred. No. 6.8e-12;
Les 62; Conservative 0; Mismatches 0;
 1.6%; Score 62; DB 5; L
100.0%; Pred. No. 7.1e-12;
ive 0; Mismatches 0;
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2000US-0211314P.
2000US-0219007P.
2000US-0255281P.
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                                   Conservative
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Query Match
Best Local Similarity
Matches 62; Conser
                                                                                                                                    1697 TA 1698
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09-JUN-2000;
18-JUL-2000;
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AAI90783 standard; cDNA; 345
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Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 56419.
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                                                                                                                                                               ABV56428 standard; cDNA; 381 BP.
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                    TG 1825
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16-MAR-2000; 2
25-MAY-2000; 2
09-JUN-2000; 2
18-JUL-2000; 2
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                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 10843.
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18-MAY-2000; 2000US-00577409.
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RESULT 28

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) salecting a composation for inhibiting prostate cancer in a patient; (f) assessing the prostate cal carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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.00.0%; Pred. No. 9.7e-0
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pharmacogenomic marker; gene;
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2000US-0189862P.
2000US-0207454P.
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18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200164835-A2
                                                              WC200160860-A2.
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                                                                                                                                                                                16-MAR-2000;
25-MAY-2000;
                                 Homo sapiens
                                                                                                                                                              17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001
                                                                                            23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA183050;
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Human, prostate cancer, prostate cancer antigen, detection, diagnosis; neuroprotective, cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilnfective; graacological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; ardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                               the encoded proceins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polympetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopolisals regulating activity, issue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                              diagnosing
                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate cancer antigen nucleotide sequence SEQ ID NO:395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3110; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 1.3%; Score 50; DB 4; Length 449; Local Similarity 100.0%; Pred. No. 9.5e-08; les 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 449 BP; 184 A; 55 C; 100 G; 109 T; 0 U; 1 Other;
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                 26-FEB-2001; 2001WO-US004927.
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ROSEN C A.
                                                 28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                          Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2001 (first entry)
                                                                                                                                                                          WPI; 2001-514838/56.
                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                             P-PSDB; AAO03119
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                                                                                                                                        Tang YT,
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(ROSE/)
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Gaps

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Length 424;

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(OXFO-) OXFORD BIOMEDICA UK LTD.
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05-OCT-2001; 2001GB-00024037.
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P-PSDB; ADD18823.
                                                       WPI; 2000-587513/55
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les 50; Conserv
                                                                                   P-PSDB; AAB56757
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   Rosen CA,
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AC ADD1
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XX ADD1
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This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention such as tumourigenesis, angiogenesis, apoptosis, inflammation, earthropotasis, or the bological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, gluconeogenesis, glucose transportation, catecholamine synthesis, into transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of
            New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a disease related protein encoding DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cervical cancer; cervical cancer marker; cancer therapy; detection; gene therapy; vaccine; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cervical cancer cell marker encoding cDNA SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1820 BP; 451 A; 485 C; 472 G; 412 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-08;
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7,3e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 50; DB
100.0%; Pred. No. 7.3
:ive 0; Mismatches
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                                                                                                                                 Claim 27; SEQ ID NO 256; 424pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlegel R, Chen Y, Zhao X, Monaha
Gannavarapu M, Glatt K, Hoersch S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACF12861 standard; cDNA; 3602
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13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 50; Conservative
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                                                                                      wound healing
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                                                                                                          Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer.
                                                                                                                                                                                                                                                  AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnerary; gene therapy; hypoxia-regulated condition; tumourigenesis; angiogenesis; apoptosis; inflammation; erythopoiesis; glycolysis; gluconeogenesis; glucose transportation; catecholamine synthesis; iron transport; nitic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 50; DB 3; Length 170
100.0%; Pred. No. 7.3e-08;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human disease related protein DNA sequence SeqID256.
                                                                                                                                                                                                            Claim 1; Page 885; 2338pp; English.
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Ruben SM;
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New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.

ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)

Claim 1, Page 218-219; 386pp; English.

Mundy CR;

Naylor S,

Harris RA,

Ward NR,

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Gapa

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given in ABR92047 to ABR92164. A higher level of expression of (1) than normal indicates the presence of cervical cancer. Also described: (1) assessing (11) containing (1); and assessing (11) containing (1); and (3) assessing (M1) whether a patient is afflicted with cervical cancer, comprising comparing the level of expression of a marker in a patient's sample, and the normal level of expression of the marker in a control non-cervical cancer sample, where a significant increase in the level of expression of the marker in the patient's sample relative to that in the cortrol sample is an indication that the patient is afflicted with cervical cancer. (1) has gycostatic activity, and can be used in gene therapy and in vaccines. (1) is useful in detecting, characterising, therapy and in treating human cervical cancers. (1) may also be used in warious prognostic and diagnostic assays, pharmacogenomics and in
                                           8 \pm 6 \pm 6
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Gaps ö Sequence 3602 BP; 790 A; 1062 C; 1017 G; 730 T; 0 U; 3 Other; Length 3602; Indels 1.3%; Score 50; DB 7; Le 100.0%; Pred. No. 6.3e-08; ative 0; Mismatches 0; DB 7; Local Similarity 100. 1es 50; Conservative Query Match Matches ઠ g

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AAX87412 standard; cDNA; 3607

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AAX87412;

(first entry) 08-OCT-1999 Hepatocellular carcinoma marker gene L4 cDNA.

Hepatocellular carcinoma; tumour; cancer; diagnosis; marker; probe; human; hepatitis B virus; x antigen; HBxAg; L4 gene; ss.

Homo sapiens

WO9939200-A1 05-AUG-1999

99WO-US001894. 27-JAN-1999;

98US-0072938P 29-JAN-1998; (UYJE-) UNIV JEFFERSON THOMAS

Feitelson MA;

WPI; 1999-469371/39.

New method for diagnosing hepatocellular carcinoma.

Claim 3; Page 43-44; 52pp; English

This sequence represents a gene, designated L4, whose expression is activated in human hepatoblastoma HepG2 cells in the presence of hepatitis B virus x antigen (HBXAg) compared to expression in HepG2 cells in the absence of HBXAG. The full-length cDNA was obtained from HepG2 cells using 5' and 3' RACE. No sequence homology was found between L4 and any previously known sequence. Synthetic peptides that represent probable antigenic determinants of the L4 protein are provided in AAY06538 and AAY06539. L4 is 1 of 10 genes (see AAX87402-11) that were initially identified by PCR select CDNA subtraction as showing differential expression in HBXAg(+) and HBXAg(-) cells. It can be used as a molecular marker for hepatocellular carcinoma (HCC). In a claimed method for marker for hepatocellular carcinoma (HCC). In a claimed method for letecting HCC, a liver tissue sample is obtained from a patient, and the level of expression of 1 or more marker genes, such as L4, in the sample is assessed. A reduction in the level of expression of the marker genes

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in the sample as compared to the expression level in noncancerous liver tissue is indicative of HCC. The method allows screening for the risk of disease and early diagnosis before tumours develop
                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                              Gaps
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                                       Sequence 3607 BP; 875 A; 938 C; 1058 G; 736 T; 0 U; 0 Other;
                                                                                                Length 3607;
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                                                                   6.3e-08;
                                                                                                                                                                                                                          Human prostate expression marker cDNA 48226.
                                                          1.3%; Score 50; DB 100.0%; Pred. No. 6.3 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                     17-FEB-2000; 2000US-0183319P.
16-WAR-2000; 2000US-0189862P.
25-WAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-021314P.
18-JUL-2000; 2000US-0219007P.
                                                                                                                                                                   ABV48235 standard; cDNA; 265
                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001WO-US005171
                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2000; 2000US-0255281P
                                                                                                                                                                                                        (first entry)
                                                    Query Match
Best Local Similarity 100.0
Watches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlegel R,
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                                                                                                                                                                                       ABV48235
                                                                                                                                                RESULT 35
ABV48235
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ö The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is a fillicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastesized in a patient; (s) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker Gaps ö Length 265; 0; Indels Sequence 265 BP; 159 A; 27 C; 31 G; 48 T; 0 U; 0 Other; Query Match
1.3%; Score 49; DB 5; Lo
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 49; Conservative 0; Mismatches 0;

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

Claim 1; Page 9463; 11750pp; English.

RESULT 36

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity elating to prytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification, but was obtained in electronic for WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4505; 1399pp + Sequence Listing; English
                                                                                                      Human polynucleotide SEQ ID NO 4505.
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514838/56.
P-PSDB; AAO04514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                               WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directly from
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ78073;
                     AAI84445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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ID ABZ7

XX AC ABZ7

XX DT 22-A

DT 22-A

DE Huma

XX Huma

XX Huma

XW Gene

KW Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                     Human, prostate cancer, cytostatic; carcinogen, pharmacodyanamic marker, pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 287 BP; 147 A; 29 C; 29 G; 50 T; 0 U; 32 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 49; DB 5; Le
100.0%; Pred. No. 2.3e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 18442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 3040-3041; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0183319P.
2000US-0189862P.
2000US-0207454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                           ABV18451 standard; cDNA; 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US005171.
                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
                                                                                                                                                                                                                                                                    13-SEP-2002
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                              Human; breast specific nucleic acid; BSNA; breast; cytostatic; gene therapy; vaccines; lung cancer; breast cancer; breast specific polypeptide; BSP; gene; ss.
                                                                                                                   94
                                                                                     Length 381;
                                                          0; Indela
Sequence 381 BP; 154 A; 66 C; 81 G; 80 T; 0 U; 0 Other;
                            DB 4; Le
                                    100.0%; Pred. ...
                               Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                Human breast specific nucleic acid #87
                                                                                                                                                                                           ABZ78073 standard; cDNA; 476 BP
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BP.

AAI84445 standard; cDNA; 381

RESULT 37

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AAI84445 ID AAI8

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The invention relates to a novel isolated breast specific nucleic acid molecule. The polypeptides of the invention have cytostatic activity. The movel nucleic acids and polypeptides may have a use in gene therapy, and as vaccines. The breast specific nucleic acid and polypeptide are useful for diagnosing and monitoring the presence and metastases of lung cancer. In a patient. The antibody that specifically binds to the breast specific polypeptide is useful for determining the presence of a breast specific polypeptide is useful for determining the presence of a breast specific portein in a sample, as well as for treating a patient with breast cancer. particularly by inducing an immune response against the breast cancer cell expressing the breast specific nucleic acid molecule or useful for identifying diagnosing, monitoring, staging, inaging and treating breast cancer and non-cancerous disease states in breast tissue. These are also useful in gene therapy, production of transgenic animals and cells, and in the production of engineered breast tissue for treatment and research. The sequences shown in AB277987-ABZ78101
                                                                                                                                                                                                                                                                                           New breast specific genes and proteins, useful in gene therapy or as vaccines for treating breast cancer or non-cancerous breast diseases, as well as for diagnosing, monitoring or staging these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expression marker cDNA 58264.
                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 198-199; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV58273 standard; cDNA; 497 BP
                                                                                                             20-NOV-2001; 2001WO-US045151
                                                                                                                                             20-NOV-2000; 2000US-0249992P
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                                                                                                                                                                                                                Macina RA,
                                                                                                                                                                              (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                               WPI; 2002-713379/77.
                                            WO200268645-A2
               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                               06-SEP-2002
                                                                                                                                                                                                              Salceda S,
Turner LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent invention
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Matches
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                                    1.3%; Score 49; DB 6; Length 476;
100.0%; Pred. No. 2.1e-07;
tive 0; Mismatches 0; Indels
Sequence 476 BP; 116 A; 88 C; 90.G; 182 T; 0 U; 0 Other;
                                                   Local Similarity 100.
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Gaps

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1.3%; Score 49; DB 5; Length 497; 100.0%; Pred. No. 2.1e-07; tive 0; Mismatches 0; Indels

49; Conservative

Matches

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Local Similarity

Query Match

Sequence 497 BP; 235 A; 77 C; 69 G; 115 T; 0 U; 1 Other;

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (e) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

Claim 1; Page 11189; 11750pp; English.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

16-MAR-2000; 2000US-0189862P. 25-MAY-2000; 2000US-0207454P. 09-JUN-2000; 2000US-0211314P.

17-FEB-2000; 16-MAR-2000;

18-JUL-2000; 2000US-0219007P.

20-FEB-2001; 2001WO-US005171.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Liu C;

Sun Y,

Cafferkey R,

Recipon H,

WO200160860-A2

23-AUG-2001

/*tag= a /*t Human; brain; Alzheimer's disease; diagnosis; antibody; expression; ds. Alzheimer's disease DNA sequence from plasmid pGCS1180. AAT72173 standard; cDNA to mRNA; 882 Socation/Qualifiers 96WO-JP003630 95JP-00322745 (first entry) 25-FEB-1998 Homo sapiens 12-DEC-1996; 12-DEC-1995; 409721807-A1 19-JUN-1997 AAT72173; RESULT 40

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5-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                     요
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                                                                                                                                                           The present sequence represents a DNA fragment which is complementary to mRNA sequences whose level of expression in the brains of Alzheimer's disease patients varies from normal individuals. The present sequence represents a specifically claimed DNA fragment in which the expression is augmented to at least twice that in normal cases. The sequence, and antibodies to the proteins encoded by the sequence, may be used in the diagnosis, treatment and investigation of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antibabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiinugal; antiparasitic; cardiant; gene therapy; food additive; preservative; chromosome identification; cancer; immune disorder; cardiovascular disorder; neurological disease;
                                                                                                DNA sequences with varied expression in normal and Alzheimer patients used for diagnosis and treatment of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                              Sequence 882 BP; 306 A; 134 C; 142 G; 300 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                         1.3%; Score 49; DB 2; Length 882;
.00.0%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                   0; Indels
                                    Zhao N, Hashida H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 47 SEQ ID NO:57.
                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune disorder; cardiovascular disord
wound healing; infectious disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis G;
                                                                                                                                      Claim 3; Page 48-49; 90pp; Japanese
                                    Kuga T, Nakagawa S, Sakaki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC79727 standard; cDNA; 903 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0126503P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity luv...
Best Local 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-594637/56.
                                                              WPI; 1997-332779/30.
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                                                                          P-PSDB; AAW19950
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17-DEC-1999;
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The polymucleotide sequences given in AAC79681 to AAC79730 encode the human secreted proteins given in ABB44595 to AAB44645. AAB44646 to AAB44693 represent human secreted polypeptide sequences and proteins howelogous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; noorcropic; neuroprotective; antivital; or unitallergic; hepatotropic; antidiabetic; antifundation; antibuleary; anticonvulsant; antidiabetic; antifundation; antiparasitic; and cardiant. The polymucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits; goats, horses, cas, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities; The polymucleotides are useful for chromosome identification. They are also useful as probes for diagnosing and ovarian cancer. They are also useful in the gene therapy of breast and ovarian cancer. The nucleic acids, protein, antibodies, agonists and antegonists from the present invention are useful in the diagnosis, treatment and prevention of: cancer; immune disorders; and in the ARC79672 to AAC79680 and AAB4455 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 903 BP; 350 A; 162 C; 173 G; 218 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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100.0%; Pred. No. 1.8e-07;
ttive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-US026524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-235357/24.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CXSXTTTXBBXBXBXBXBXBXBXBXBXBXBXBXCXX
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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens have extosteratic activity and can be used in gene therapy cancer antigens have extosteratic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. Additionally and Additionally sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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Gaps ö Sequence 1057 BP; 318 A; 210 C; 207 G; 320 T; 0 U; 2 Other; Length 1057; 0; Indels 1.3%; Score 49; DB 4; Le 100.0%; Pred. No. 1.8e-07; ative 0; Mismatches 0; Local Similarity 100. Query Match Matches

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AAC79719 standard; cDNA; 1263

12-FEB-2001 (first entry) AAC79719;

Human secreted protein gene 39 SEQ ID NO:49,

Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatorropic; antidiabetic; antifinamatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; food additive; preservative; chromosome identification; cancer; immune disorder; cardiovascular disorder; neurological disease; wound healing; infectious disease; se:

Homo sapiens.

WO200058339-A2.

05-OCT-2000.

22-MAR-2000; 2000WO-US007440

99US-0126503P. 99US-0172409P. 26-MAR-1999; 17-DEC-1999; (HUMA-) HUMAN GENOME SCI INC

Komatsoulis G; Rosen CA, Ruben SM,

WPI; 2000-594637/56. P-PSDB; AAB44634. Fifty nucleic acid molecules encoding human secreted proteins, the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.

Claim 1; Page 360; 410pp; English

The polynucleotide sequences given in AAC79681 to AAC79730 encode the human secreted proteins given in AAB44596 to AAB44645. AAB44646 to

Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM; WPI; 2000-587533/55. P-PSDB; AAB43407.

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AAB44693 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: Cytostatic; immunosuppressive; noorropic; neuroprotective; antivital; antivities include: Cardiant. The genes are thindiabetic; antifuflamatory; antivital; vulnerary; anticonvulsant; antidabetic; antifuflamatory; antiparasitic; and cardiant. The polymucleotides and polypeptides are useful for preventing, trabite; goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polymucleotides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, particularly breast and ovarian cancer. They are also useful in the gene therapy of breast and ovarian cancer. The mucleic acids, protein, antibodies, agonists and and ovarian the present invention are useful in the diagnosis, treatment and prevention of: cancer; immune disorders; cardiovascular AC79672 to AAC79680 and AAB44955 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitheumatic; antiarthritic; antintral; antinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaquiant; nootropic; vasorropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haematotolytic; cardiovascular disorder; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1263 BP; 306 A; 383 C; 323 G; 245 T; 0 U; 6 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 49; DB 3; Le
100.0%; Pred. No. 1.7e-07;
cive 0; Mismatches 0;
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nes 49; Conservative
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB43399. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiathmatic; antidabetic; antiathmatic; antidabetic; antiathmatic; antidabetic; antiphromic; antidabetic; antiphromic; antidabetic; antiphromic; antidabetic; cardial; thrombolytic; cagulant; dermatological; neuroprotective; cardiant; thrombolytic; cagulant; nootropic; vascropic; antiphromic; and antiangiogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Collymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune collers, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and abcrerial or viral infections. The present shorty screens. AAC78449 to AAC78457 and antagonists may be also be used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birnbaum D, Nguyen C, Viens P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1373 BP; 398 A; 362 C; 370 G; 241 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 3; Le
Pred. No. 1.7e-07;
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                 Claim 1; Page 616-617; 2352pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention
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Claim 1; Page 130-131; 401pp; English.

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Gaps . 0

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Length 1373;

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The present invention describes a polynuclectide library (I) useful in the molecular characterisation of a carcinoma, comprising a pool of polynuclectides or its subsequences which are either underexpressed or overexpressed in tumour cells, and correspond to any of the polynuclectide sequences given in ABV94010 to ABV94447. Also described: (I) a polynuclectide array (II) useful for the prognosis or diagnostic of tumour, comprising (I); and (2) detecting (MI) differentially expressed polynuclectide sequences which are correlated with a cancer, involves obtaining a polynuclectide sample from a patient, and reacting the polynuclectide sample obtained with a probe immobilised on a solid support, where the probe comprises any combination of the polynuclectide sequences of (I) or its expression product of the polynuclectide sequences of (I), and detecting the reaction product (I) have cycostatic activities and can be used as anti-tumour agents. (I) are useful in molecular characterisation of a carcinoma. (I) and (II) are useful for the prognosis or diagnostic of tumour, in differentiating a normal cell, differentiating a tumour with lymph nodes from a tumour without commal cell from a cancer cell, detecting a hormone sensitive tumour cell, mand a netracycline-sensetive tumours. (I) is useful for large-scale molecular characterisation of breast cancer that help in prediction, prognosis and cancer treatment, and for detecting differentially expressed genes that cancer certacted with a cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1429 BP; 372 A; 384 C; 381 G; 292 T; 0 U; 0 Other;
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Pred. No. 1.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prea. w..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH72649 standard; cDNA; 1676 BP
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14-MAX-2000; 2000US-0189315P.
112-MAX-2000; 2000US-0203791P.
09-UTN-2000; 2000US-0210600P.
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Best Local Similarity 100.
Matches 49; Conservative
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                        The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
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pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1676;
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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Matches
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ABV27467

ABV27
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                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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               Sequence 1702 BP; 560 A; 309 C; 393 G; 440 T; 0 U; 0 Other;
                                              Length 1702;
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                                              DB 5; Le
1.6e-07;
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100.0%; Pred. No. 1.6e-07;
ive 0; Mismatches 0;
                                  1.3%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 27715.
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And 49; Conservative
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                                                                             49; Conservative
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                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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RESULT 49

ABV25281

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytostatic; diagnosis; prostate disorder; prostate cancer; BPH; benign prostatic hyperplasia; SAP-1 protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1702 BP; .560 A; 309 C; 393 G; 440 T; 0 U; 0 Other;
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1.6e-07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA encoding SAP-1 protein (marker 20)
                                           Human prostate expression marker cDNA 21884.
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00.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                              2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
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(first entry)
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Best Local Similarity 100.
Matches 49; Conservative
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                                                                                                                                                                                          WO200160860-A2
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25-MAY-2000;
09-JUN-2000;
                                                                                                                                                     Homo sapiens
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  13-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer. (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (e) selecting a compound to inhibit prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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1.6e-07;
                                                                                                                                                                                                                                    Human prostate expression marker cDNA 25272.
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100.0%; Pred. No. 1.6
ative 0; Mismatches
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                                                                                                       ABV25281 standard; cDNA; 1702
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25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-021314P.
18-UUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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                                                                                                                                                                                          (first entry)
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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Homo sapiens

ABV21893

ABV21893 ID ABV2 XX AC ABV2

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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancerassociated polymucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancerassociated polymucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that thibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                   Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytostatic; gene therapy; inflammatory disorder; neural disorder; Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; muscular disorder; ischaemia; reproductive disorder; Crohn's disease; pulmonary disorder; sancer; myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour; haematopoietic disorder; rhinitis; asthma; diabetes; atherosclerosis; anti-sense therapy; endocrine disorder; leukaemia; ss.
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/product= "Human novel protein"
/note= "CDS does not include start codon"
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                                                                                                             Hevezi P;
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. No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 416; 436pp; English.
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                                                                                                           Wilson KE,
                                                                  (EOSB-) EOS BIOTECHNOLOGY INC.
30-APR-2001; 2001US-00847046. 04-MAY-2001; 2001US-0288589P.
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/partial
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P-PSDB; ABG61934.
                                                                                                           Mack DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses a method for diagnosing, prognosing or monitoring a prostate disorder which involves the analysis of 26 gene transcripte (referred as markers) that exhibit bebrant expression levels in prostate disorder tissues and provides a means of early diagnosis. This method is useful for diagnosing, prognosing or monitoring a prostate disorder. It also provides a means of distinguishing prostate cancer from benign prostatic hyperplasia (BPH) and for identifying potential anti-prostate disorder. It disorder therapeutic compounds. The present sequence is a human DNA encoding SAP-1 protein (referred as marker 20). The SAP-1 protein is identified as a protein recruited by serum response factor to the c-fos
                                                                                                                                                                                                                                                                                                                                   Diagnosing and monitoring prostate disorders, by analysis of 26 gene transcripts that exhibit aberrant expression levels in prostate disorder tissues, and provides a means of early diagnosis.
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2000US-00733288.
2000US-0073342.
2001US-0263957P.
2001US-0276791P.
2001US-0216888P.
2001US-0281922P.
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                                                                                     08-NOV-2000; 2000WO-GB004267.
                                                                                                                                  99GB-00026805
                                                                                                                                                                           (ASTR ) ASTRAZENECA AB.
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                                                                                                                                                                                                                                                                                           WPI; 2001-343837/36.
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WO200136674-A2.
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16-MAR-2001;
16-MAR-2001;
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24-APR-2001;
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ADS 25

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17-JAN-2001; 2001WO-US001325
02-AUG-2001
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2000US-0246523P 2000US-0246524P 2000US-0246524P 2000US-0246528P 2000US-0246532P 2000US-0246532P 2000US-0246632P 2000US-0246610P 2000US-0246610P 2000US-0246610P 2000US-024920P 2000US-0249210P 2000US-0249210P 2000US-0249214P 2000US-0249214P

(HUMA-) HUMAN GENOME SCI INC.

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                                                                                                                                                               Isolated polypeptide for treating, preventing and/ or prognosing medical disorders and also for testing and detection e.g. diagnosis and screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen; respiratory-Gen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD16750-AAD16775 represent cDNAs corresponding to novel human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%; Scor. No. 1.00.0%; Pred. N
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 19; 469pp; English.
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2000US-0186350P.

2000US-0189874P.

2000US-0190076P.
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Best Local Similarity 100.0
Matches 49; Conservative
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WPI; 2001-451925/48.
P-PSDB; AAE09698.
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02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                for agonists.
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PR 79-WRY-2000; 2000US-0205651EP.
PR 70-UUN-2000; 2000US-021868EP.
PR 30-UUN-2000; 2000US-021186EP.
PR 10-UUN-2000; 2000US-021186EP.
PR 11-UUL-2000; 2000US-021186EP.
PR 11-UUL-2000; 2000US-021255EP.
PR 11-UUL-2000; 2000US-02125FP.
PR 21-SEP-2000; 2000US-02125F
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                                                                                                                                                                                                                                                                                          New nucleic acid molecules and polypeptides for diagnosing, preventing or treating disorders associated with aberrant expression of the polypeptide, e.g. neural or cardiovascular disorders, and in chromosome identification.
                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule (cDNA)
                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 19; 242pp; English
                                                                                      2000US-0246609P.
2000US-0246610P.
2000US-0246611P.
2000US-0249207P.
2000US-0249208P.
2000US-0249208P.
                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                     17-JAN-2001; 2001US-00764903
                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                               WPI; 2003-786903/74.
P-PSDB; ADC22076.
           20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
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                                                             08-NOV-2000,
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08-NOV-2000
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                                                                               08-NOV-2000
                                            08-NOV-2000
                                                         38-NOV-2000
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cencoding a human secreted protein, representing one of 15 novel genes.

Also included are recombinant vectors, host cells (expressing the protein), the secreted proteins (including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological a condition based on the presence or absence of the mutation), diagnosing a pathological condition or susceptibility to a pathological condition of susceptibility to a pathological condition of comprising determining the presence or amount of expression of the protein in a biological sample and diagnosing a condition of the protein in a biological sample and diagnosing a condition or ameliorating medical condition by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the protein to a mammalian subject, identifying a binding partner to the protein to a mammalian subject, identifying a binding partner to the protein to a mammalian subject, comprising expressing the nucleic acid in a cell, isolating the supernatant having the activity) in a biological assay of the protein in the supernatant having the activity). The nucleic acids the protein display the following activities Cytostatic, antibacterial, virucide, Neuroprotective, Gynaecological, Gastroincestinal-Gen, Cardiant, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Funke RP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.3%; Score 49; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACD13422 standard; cDNA; 2038
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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P-PSDB; ABO07249.
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ACD13422
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Claim 2; Page; 266pp; Japanese.

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modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or muclaic acid with a test agent under conditions, where but for the presence of the test agent bushed activity of the assay system. Corresponding a rest agent-biased activity of the assay system. Also included are modulating (MA) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway of a disease in a patient (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosting (Specifically binds an HM polypeptide or nucleic acid) and diagnosting (Comparising contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparing the results with a probe for HM expression contacting the patient; (b) contacting the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where disease, of the p53 pathway, such as, angiogenesis, apoptotic or cell to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell confideration of the cell, so that the cell undergoes normal confidence or also useful for modulating the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, also useful for treating defects. The present sequence is an HM collect acid encoding a p53 pathway modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2038 BP; 527 A; 580 C; 567 G; 364 T; 0 U; 0 Other;
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ö ö 1.3%; Score 49; DB 7; Length 2038; 100.0%; Pred. No. 1.6e-07; 100.0%; Prec. ... Conservative Local Similarity 49; Query Match Best Loca Matches ò g

ABZ71965 standard; cDNA; 2106 BP. ABZ71965; RESULT 56

01-APR-2003 (first entry)

Human cDNA for transketolase GenBank X67688

Human; cancer; stomach cancer; cytostatic; gene; ss.

Homo sapiens

WO200283899-A1.

24-OCT-2002.

10-APR-2001; 2001JP-00112039. 21-SEP-2001; 2001JP-00290193. 28-MAR-2002; 2002WO-JP003038.

(TAKA-) TAKARA BIO INC

Mineno J, Asada K, Oura I, Okamoto S, Mori M; Yoshikawa Y, Inoue H,

Kato I;

WPI; 2003-093022/08

Measuring changes in expression of 264 cancer associated genes for detection of stomach cancer and screening of potential anticancer agents.

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                            The invention relates to a method for the detection of cancer in which a change in the expression of 1 or more of 264 specified cancer associated egenes, ABZ71694-ABZ71657, or of sequences at least 80% homologous to them in the specimen tissue as compared to normal tissue is observed. The genes are used in detection, diagnosis and treatment of cancer, especially of stomach cancer. The present sequence is that of a cancer associated polymucleotide of the invention. Note: The present sequence was not given in the printed specification but was isolated using the Genbank accession number given in the DE line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynuclectides 95% identical to the sequences of the invention. The invention additionally relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertibility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; ene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antinflammatory; gynaecological; reproductive; chromosome 3p14.3; gene;
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                              Sequence 2106 BP; 529 A; 608 C; 589 G; 380 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 1.3%; Score 49; DB 7; Length 2106; 100.0%; Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian antigen HAZAA31 cDNA, SEQ ID NO:740.
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.60
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ54860 standard; cDNA; 2143 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-147878/19.
P-PSDB; ABP41783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birse CE, Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ54860;
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ABQ54860/
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30-MAR-2000; 2000US-00540763

polynucleotides, antibodies against human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of of orwarian antigen polynucleotides and polypeptides; in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system (alsorders (e.g., infertiolty, disorders of pregnancy, ancoulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea, endocrine disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders antimucodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), lood-related disorders (e.g., anaemia), cardiovascular disorders and uninary system disorders. Ovarian antigen polypeptides and modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present of sequence represents conditions or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present compensation of individuals and in foremic analysis, and the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the printed specification, but was obtained per electronic format directly from the printed specification, but was obtained per electronic format directly from the printed specification, but seed sequences. Sequence 2143 BP; 377 A; 598 C; 620 G; 545 T; 0 U; 3 Other; 88888888888888888888888888888888

Gaps 0; Query Match .1.3%; Score 49; DB 6; Length 2143; Best Local Similarity 100.0%; Pred. No. 1.6e-07; Matches 49; Conservative 0; Mismatches 0; Indels ઠે

AAC76644 standard; cDNA; 2543 BP

08-FEB-2001 (first entry)

Human ORFX ORF2199 polynucleotide sequence SEQ ID NO:4397.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

Wulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective;

Wulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective;

Muticonvulaant; otheropathic; coagulant; vasotropic; antidiabetic;

Mypotensive; dermatological; immunosuppressive; antidiabetic;

Mypotensive; dermatological; immunosuppressive; antidiabetic;

Mutiviral; antibacterial; antifungal; antiheumatic; antidhyroid;

antianaemic; gene therapy; cancer; proliferative disorder; hypetension;

metrodegenerative disorder; osteoarthritis; graft vs host disease;

metrodegenerative disorder; osteoarthritis; hypothyroidism; SID; AIDS;

cholesterol ester storage; systemic lupus erythematosus; infection;

severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

mallergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

bone damage; cartilage damage; antiinflammatory disease; coagulation;

thrombosis; contraceptive; ss.

Homo sapiens.

40200058473-A2

05-OCT-2000

31-MAR-2000; 2000WO-US008621.

99US-0127607P. 99US-0127636P. 99US-0127728P. 02-APR-1999; 05-APR-1999; 31-MAR-1999;

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; valnerary; antipporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporial; thrombolytic; antiparkinsonian; nootropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antihiflammatory; antibacterial; antiviral; antifthugal; antithreumatic; antithyroid; antibacterial; antithreumatic; antithyroid; antibacterial; to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegemerative clastores, proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegemerative disorders, osteoarthritis, graft we host disease, cardiovascular disease, disorders, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplandal infection, malaria, autoimmune cartilage damage, noctural hemoglobinutia, antinflammatory disease; to Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease. enhance coagulation; to inhibit thrombosis; and as a contraceptive 1.3%; Score 49; DB 3; Length 2543; 100.0%; Pred. No. 1.5e-07; rative 0; Mismatches 0; Indels Sequence 2543 BP; 630 A; 589 C; 684 G; 639 T; 0 U; 1 Other; Claim 5; Page 3587-3589; 5507pp; English Best Local Similarity 100. Matches 49; Conservative Shimkets RA, Leach M; (CURA-) CURAGEN CORP. P-PSDB; AAB42435 Query Match \$X454X4X4X44444X8X8X8X444X4X4X4X4X4X

AAD43556 standard; cDNA; 2713 BP 14-NOV-2002 (first entry) Human CD2000 cDNA. AAD43556; RESULT 59 AAD43556 요

Gaps

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Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; carcinoma, autoimmune disorder; immune disorder; rheumatoid arthritis; carcinoma, autoimmune disorder; multiple sclerosis; Grave's disease; Grave's disease; psociasis; grave's disease; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psociasis; apported inflammatory disorder; viral infection; asthma; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antiinflammatory; Crohn's disease; osteopathic; antibacterial; immunomodulator; inflammatory; ocoh; disease; aundice; dermatological; ulcerative colitis; AIDS; chromosome 1q23; gene; ss

Homo sapiens

us-10-005-907-1.oligo.rng

(first entry)

14-NOV-2002

Human CD2000 DNA #3.

/*rag= d /note= "This region designated as SEQ.ID.NO:2 is specifically referred in claim 2"

/*tag= a /product= "Human CD2000 protein"

.1056

socation/Qualifiers

.1059

/*tag= c /product= "Human mature CD2000 protein"

/*tag= b 130. .1056

.129

Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carctinoma; autocimmune disorder; multiple solerosis; Grave's disease; Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psoriasis; apoptotic disorder; systemic lupus erythematorsus; bronchitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; meuroprotective; antinflammatory; Crohn's disease; osteopathic; antibacterial; immunomodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AlDS; gene; ds.

Ното варіелв

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Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
                                                                                                                                                                                                  Claim 1; Page 66; 138pp; English
                                                                                                          02-NOV-2001; 2001EP-00309339.
                                                                                                                      03-NOV-2000; 2000US-00706167
                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                         WPI; 2002-620680/67.
P-PSDB; AAE26220.
                        misc_feature
                                                                                   EP1223218-A1
                                                                                              17-JUL-2002
                                              sig_peptide
                                                           mat_peptide
                                                                                                                                             Fraser CC;
Key
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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (1g) and 1g-like domains and SAM associated protein (SAP) motifie. CD000 DNA and protein is useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Graves disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. treumatoid arthritis and colitis), inflammatory disorders (e.g. treumatoid arthritis and colitis), inflammatory disorders (e.g. systemic lupus erythematosus, and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytocoxic disorders, septic shock, cinsulin-dependent diabetes mellitus), cytocoxic disorders, septic shock, corronic obstructive pulmonary disease (e.g. emphysema), bronchtis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in gene therapy. CD2000 DNA is useful in screening assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical therapeutic and prophylactic). The present sequence is human CD2000 DNA. Human CD2000 gene is located at chromosome 1q23
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                                        Gaps
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Length 2713;
                                      0; Indels
Query Match
1.3%; Score 49; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 49; Conservative 0; Mismatches 0;
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ð g RESULT 60 AAD43566 ID AAD43566 standard; DNA; 2713 BP. XAC AAD43566;

RESULT 61

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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. caquired immune deficiency syndrome (AIDS)), inflammatory disorders (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. asthma and psortasis), allergic inflammatory disorders (e.g. asthma and osteoarthritis), allergic inflammatory disorders (e.g. asthma and cortasis), apoptotic disorders (e.g. systemic lupus erythematosus, and provide obstructive pulmonary disease (e.g. emphysema), bronchitis, carcheria, jaundice, hepatic circulatory disorders, hepatic; shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, carcheria, jaundice, hepatic circulatory disorders, hepatic; shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, carcheria, gene therapy, CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD2000 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
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1.3%; Score 49; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-620680/67.
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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains useful fark associated protein (SAP) motifis. CD3000 DNA and protein is useful for treating disorder such as immune proliferative disorders in method of a carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple selerosis, Grave's disease, and Hashinoto's disease), T cell disorder (e.g. arcuiroders (e.g. crucinoma), viral infection, autoimmune disorders (e.g., arthritis, and disease), Inflammatory bowel disease (e.g. crohn's disease and ulcerative (AIDS)), inflammatory disorders (e.g. crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. asthma and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and psoriasis), allergic inflammatory disorders (e.g. emphysemal, bronchitis, chromic obstructive publimonary disease (e.g. emphysemal, bronchitis, carchexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anneamia. CD2000 DNA is useful in screening assays, detection assays, ed.g. chromosomal mapping, tissue typing, forensic biology), predictive (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. human CD2000 DNA therapeutic and prophylactic). The present sequence is human CD2000 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
                                                                                                                                                                                                                         Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma, autoimmune disorder; multiple sclerosis; grave's disease; Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psortasis; apoptotic disorder; systemic lupus erythematosus; bronchitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute mysloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antiniflammatory; Crohn's disease; osteopathic; antibacterial; immunosudulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AlDS; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 78; 138pp; English.
                        AAD43565 standard; DNA; 2713 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-2000; 2000US-00706167.
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                                                                                                                              14-NOV-2002 (first entry)
                                                                                                                                                                                Human CD2000 DNA #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1223218-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo, sapiens
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                                                                             AAD43565;
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Sequence 2713 BP; 798 A; 648 C; 529 G; 738 T; 0 U; 0 Other;

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Gaps
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1.3%; Score 49; DB 6; Length 2713;
100.0%; Pred. No. 1.5e-07;
ative 0; Mismatches 0; Indels
                  Best Local Similarity 100.
Matches 49; Conservative
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Novel isolated polypeptide containing immunoglobulin and immunoglobulin-like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders. Human, immunoglobulin, Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carchinoms; autoimmune disorder; multiple sclerosis; Grave's disease; Habhimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psoriasis; apoptotic disorder; systemic lupus erythematorsus; bronchtitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; dirrhosis; acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cyrostatic; immunosuppressive; neuroprotective; antiniflammatory; Crohn's disease; osteopathic; antibacterial; immunosmodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AIDS; gene; ds. AAD43564 standard; DNA; 2713 BP. 03-NOV-2000; 2000US-00706167. 02-NOV-2001; 2001EP-00309339. (MILL-) MILLENNIUM PHARM INC. 14-NOV-2002 (first entry) WPI; 2002-620680/67. Human CD2000 DNA #1 Homo gapiens EP1223218-A1 17-JUL-2002. Fraser CC; AAD43564; RESULT 62 AAD43564 ID AAD43 XX 셤

The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin [1g] and 1g-like domains useful for treating disorder such as immune proliferative disorders.

In mune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. arduired immune deficiency syndrome (e.g., arthritis, multiple sclerosis, erguired immune deficiency syndrome (albs)), inflammatory disorders (e.g. rheumatory syndrome (albs)), inflammatory disorders (e.g. rheumator) asthma and osteoarthritis), allergic inflammatory disorders (e.g. asthma and osteoarthritis), allergic inflammatory disorders (e.g. asthma and osteoarthritis), allergic inflammatory disorders (e.g. asthma and osteoarthritis), allergic inflammatory disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchtis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, cuther myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomice), and in methods of treatment (e.g. human CD2000 DNA therapeutic and prophylactic). The present sequence is human CD2000 DNA

Disclosure, Page 77-78; 138pp; English.

Sequence 2713 BP; 799 A; 646 C; 529 G; 739 T; 0 U; 0 Other;

1.3%; Score 49; DB 6; Lv 100.0%; Pred. No. 1.5e-07; Query Match Best Local Similarity

Query Match .

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Gaps

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Length 2713;

Sequence 2713 BP; 799 A; 648 C; 529 G; 737 T; 0 U; 0 Other;

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Gaps

Query Match
1.3%; Score 49; DB 6; L.
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 49; Conservative 0; Mismatches 0;

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Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
                                                                                                                                                                                                                               immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease; Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; hamophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antilinflammatory; crohu's disease; osteopathic; antibacterial; immunosupatory; crohu's disease; jaundice; dermatological; ulcerative colitis; AIDS; gene; ds.
                                                                                                                                                                                                                      Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein;
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                       0; Indels
Mismatches
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                                                                                                                 AAD43567 standard; DNA; 2713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                   (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-620680/67.
                                                                                                                                                                                            Human CD2000 DNA #4.
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                                                                                                                                                                  14-NOV-2002
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49;
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                                                                                                                                          AAD43567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser
Matches
                                                                                                    AAD43567
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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains useful for treating disorder such as immune proliferative disorders, insuline disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. captioned immune deficiency syndrome (albs), inflammatory bowel disease (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. sthma and psortiasis), allergic inflammatory disorders (e.g. suchmatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. suchmatoids, and psortiasis), allergic inflammatory disorders (e.g. suchmatoids, and psortiasis), allergic inflammatory disorders (e.g. emphysema), bronchitis, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatic; strinosis, cachexia, jaundice, hepatic circulatory disorders, hepaticis, cirrhosis, centermy, CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenemics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD2000 DNA Disclosure; Page 79-80; 138pp; English

RESULT 65

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated canine low affinity immunoglobulin E (IgB) receptor (CD23) polypeptides and encoding mucleic acid molecules. The CD23 polypeptides can be expressed by standard recombinant methodology. The CD23 polymucleotides are useful for protecting canide from diseases mediated by CD23, for developing compounds that regulate Igg and/or CD23 levels in a canid for treating allergy related diseases such as atopic dermatitis, asthma, hay fever and food sensitivities. The present sequence represents a CD23 nucleic acid molecule nCaCD23_2851
                                                                                                                                                                                                                           Canine; immunoglobulin E; IgE; CD23; antiallergic; antiasthmatic; gene; antiinflammatory; dermatological; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated canine low affinity immunoglobulin E receptor nucleic ad molecule, useful for protecting canids from diseases mediated by the receptor, such as allergy, atopic dermatitis, asthma, and hay fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                             Canine low affinity IgE receptor (CD23) nCaCD23_2851 DNA sequence.
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                           Sequence 2851 BP; 604 A; 938 C; 781 G; 528 T; 0 U; 0 Other;
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Indels
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1.3%; Score 49; DB 6; Li
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "CD23 receptor"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
199. .1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1a; Col 31-36; 33pp; English.
                                                                                                      ABN86559 standard; DNA; 2851 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0125913P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2000; 2000US-0053551
                                                                                                                                                                  05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber ER, Mccall CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-588896/63.
P-PSDB; ABB81056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                        Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                 US6410714-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-2002
                                                                                                                                   ABN86559;
                                                                          RESULT 64
                                                                                          4BN86559
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Lemieux SM;

Hu W,

Eroshkin AM,

Zamudio C,

Tishkoff D,

2001US-0297066P. 2001US-0295890P. 2001US-0303899P.

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The invention relates to novel purified or isolated nucleic acids of
essential genes of Aspergillus fundatus. The isolated nucleic acids of
the invention are used to treat or prevent infections by a pathogenic
organism such as A. fundatus, to treat a non-infectious disease in a
subject (e.g. cancer), to prevent or tontain contamination of an object
by A. fundatus, or to prevent or inhibit formation on a surface of a
by A. fundatus, or to prevent or inhibit formation on a surface of a
corporation recombinant protein for characterisation, screening or
therapeutic use, as markers for host tissues in which the pathogenic
corganisms invade or reside, for comparing with the DNA sequences of other related or distant pathogues having the same or
similar biochemical activity and/or function, for comparing with DNA
sequences of other related or distant pathogues, for selecting and
making oligomers for attachment to a nucleic acid array for examination
of expression patterns, for raising anti-protein antibodies, as an
antigen to raise anti-DNA antibodies or to elicit another immune
response, and for identifying polynucleotides encoding the other protein
with which binding occurs or to identify inhibitors of the binding
occurs or to identify inhibitors of the protein
with which binding occurs or to identify inhibitors of the protein
theraction. The polypeptides may be used to raise antibodies or to
determine lesponse, as a reagent in assays designed to quantitatively
that is now to in the pathogue in invise and and in and the content of the protein in biological fluids as a marker for
the pathogue and the protein in biological fluids as a marker for
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the pathogue and the protein in biological fluids as a marker for
the pathogue and the pathogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page; 175pp; English.
                                     23-APR-2002; 2002WO-US013142.
                                                                                                                                                                                                                                                 31-AUG-2001; 2001US-0316362P
                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-093124/08.
                                                                                                                                     27-APR-2001; 2
05-JUN-2001; 2
09-JUL-2001; 2
                                                                                                        23-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                           Jiang B,
   The invention relates to isolated canine low affinity immunoglobulin E (IGE) receptor (CD23) polypeptides and encoding nucleic acid molecules. The CD23 polypeptides can be expressed by standard recombinant methodology. The CD23 polymucleotides are useful for protecting canids from diseases mediated by CD23, for developing compounds that regulate IGE and/or CD23 levels in a canid for treating allergy related diseases such as atopic dermatitis, asthma, hay fever and food sensitivities. The present sequence represents the complementary sequence of the CD23 nucleic acid molecule nCaCD23_2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated canine low affinity immunoglobulin E receptor nucleic acid molecule, useful for protecting canids from diseases mediated by the receptor, such as allergy, atopic dermatitis, asthma, and hay fever.
                                                                                                                                                                                                                                                                                                                    Canine; immunoglobulin B; IgB; CD23; antiallergic; antiasthmatic; antiinflammatory; dermatological; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 2851; 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2851 BP; 528 A; 781 C; 938 G; 604 T; 0 U; 0 Other;
                                                                                                                                                                                                                                              Canine CD23 nCaCD23_2851 complementary DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 49; DB
100.0%; Pred. No. 1.5
vative 0; Mismatches
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                                     ABN86560 standard; DNA; 2851 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000US-00535521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber ER, Mccall CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-1999;
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                                                                                                                                                                              05-NOV-2002
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                                                                                                           ABN86560;
ABN86560/C
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AC
ABN865
XX
AC
ABN865
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ABN865
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ABN865
XX
Canine
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host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or vixulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus funigatus of the invention
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                         Length 2944;
                                                                                                       Sequence 2944 BP; 676 A; 770 C; 765 G; 733 T; 0 U; 0 Other;
                                                                                                                                             1.3%; Score 49; DB 7; Le
100.0%; Pred. No. 1.5e-07;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus essential gene #2968.
                                                                                                                                                                                                                                                                                                                                                                              ABT20610 standard; DNA; 3362 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-2003 (first entry)
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus fumigatus
                                                                                                                                                                   Local Similarity
                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                      ABT20610;
                                                                                                                                                    Query Match
                                                                                                                                                                                         Matches
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ID ABT22
XA AC ABT2
XX ABT2
XX XX ABT2
XX XX ASPE:
XX ASPE:
XX CANG:
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Pungicide, cytostatic, essential gene, Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response; ds.

Aspergillus fumigatus essential gene #1152.

RESULT 66
ABT18794/c
ID ABT18794 standard; DNA; 2944 BP.
XX
AC ABT18794;
XX
DT 16-APR-2003 (first entry)
XX
XX
KW Fungicide; cytostatic; essential genx
XX
KW Pungicide; cytostatic; essential genx
XX
KW cancer; contamination; biofilm; ann
XX
OS Aspergillus fumigatus.
XX
NO200286090-A2.
XX
XX
PD 31-OCT-2002.

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Gaps

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New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                     Disclosure; Page; 175pp; English.
                                                        27-APR-2001; 2001US-0287066F.
05-UM-2001; 2001US-029589P.
09-UUL-2001; 2001US-0303999P.
31-AUG-2001; 2001US-0316882P.
                                    23-APR-2002; 2002WO-US013142
                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                           Tishkoff D,
                                                                                                                          WPI; 2003-093124/08.
       WO200286090-A2
                                                  23-APR-2001;
                      31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                           Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus funigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. funigatus, or to prevent or inhibit formation on a surface of a carpressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA captures of other related or distant pathogenic organisms to identify contains and or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of contains and c of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polyuclectides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention Sequence 3362 BP; 774 A; 901 C; 867 G; 820 T; 0 U; 0 Other;

Gaps ö Score 49; DB 7; Length 3362; 0; Indels Local Similarity 100.0%; Pred. No. 1.4e-07; nes 49; Conservative 0; Mismatches 0; 1.3%;

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ABQ92014 standard; cDNA; 4236 ABQ92014; ABQ92014
ID ABQ
XX
AC ABQ
XX
DT 04XX
DE Hum

RESULT 68

04-OCT-2002 (first entry)

Human polynucleotide SEQ ID NO 11.

protein; immunostimulant, antiparasitic; secreted protein; transmembrane protein cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's esses esse; secoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss. Human, cytostatic, antirheumatic, antiarthritic, vulnerary, analgesic, antiliflammatory, antibacterial, immunosuppressive, antibackinsonian, eneuroprotective, noctropic, osteopathic, heamostatic, vasotropic, antiulcer, fungicide, antidiabetic, antiasthmatic, antiallergic,

Homo sapiens.

US2002065394-A1

30-MAY-2002.

Lemieux SM;

Eroshkin AM, Hu W,

Zamudio C,

22-DEC-2000; 2000US-00745763.

98US-00040963 JACOBS K. 18-MAR-1998; JACO/)

MCCOY J M. LAVALLIE E R. COLLINS-RACIE L A.

(MCCO/) (LAVA/) (COLL/) (EVAN/) (MERB/)

EVANS C. MERBERG D.

(TREA/) TREACY M. (SPAU/) SPAULDING V.

Collins-Racie LA, Evans C; Lavallie ER, Spaulding V; Mccoy JM, Treacy M, Jacobs K, Merberg D,

WPI; 2002-582343/62 P-PSDB; ABP61797.

Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.

Claim 34; Page 106-108; 284pp; English

The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic acid (CDNA) inserts (II), where the protein is aubstantially free from other mammalian proteins. (I) are useful for preventing, treating or analozating or the mammalian proteins. (I) act useful for preventing, treating or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antimiflammatory, stem cell growth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem calls in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or rise to neuroepithelial cells that can be used to augment or replace contral and peripheral nervous system diseases and neuropathies, such as Alzaeimer's, Parkinson's disease, Huntington's disease, anyotrophec central and peripheral nervous system diseases and neuropathies, such as Alzaeimer's, Parkinson's disease, Huntington's disease, anyotrophec activity, regulation of haemacopolesis and is useful for treating weloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of hone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, uncertaing osteoporosis, osteoarthritis, bone degeneration of severe combined insunodeficiency (SCID), bacterial or fungal infections, a various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, dabetes mellitus, myasthenia gravis, allergic reactions and conditions, crecombinant protein, as markers for tissues in which the corresponding crecombinant protein, as markers for tissues in which the corresponding sequence is that of a polymucleotide of the invention

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Gaps

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Length 4236; 0; Indels

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The invention relates to novel purified or isolated mucleic acids of essential genes of Aspergillus funigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic organism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. funigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. funigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic corganism invade or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA corporates of or of distant pathogenic organisms to identify operatial orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for rasising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune cours or to identify inhibitors of the binding circurs or to identify inhibitors of the binding circurs or to interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                  Sequence 4236 BP; 1330 A; 778 C; 784 G; 1338 T; 0 U; 6 Other;
                                                                       Query Match 1.3%; Score 49; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene #558
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 69
ABT18200/C
ID ABT18200,
XX
AC ABT18200;
XX
I6-APR-2003 (first entry)
XX
Aspergillus fumigatus essential ge
XX
Aspergillus fumigatus essential ge
XX
Aspergillus fumigatus.
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Aspergillus fumigatus.
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Aspergillus fumigatus.
XX
WC200286090-A2.
XX
WC200286090-A2.
XX
WC200286090-A2.
XX
D1-CCT-2002.
XX
XX
ADT1-2001; 2001US-0285697P.
PR 23-APR-2001; 2001US-02850P.
PR 23-APR-2001; 2001US-02001; 2001US-02850P.
PR 23-APR-2001; 2001US-02850P.
PR 23-APR-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page; 175pp; English.
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Hu W,

Eroshkin AM,

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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. funigatus, to prevent or inhibit formation on a surface of a corporation comprising A. fumigatus. The polymucleotides are useful for expressing recombinant protein for characterisation, screening or thraspeutic use, as markers for host tissues in which the pathogenic organisms invide or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify making oligomers for attachment to a nucleic acid array for examination making oligomers for attachment to a nucleic acid array for examination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fungicide, cytostatic, essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response; ds.
host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polymuclectide sequence represents one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                    Gaps
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                                                                                                     Seguence 4944 BP; 1177 A; 1248 C; 1244 G; 1275 T; 0 U; 0 Other;
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                                                                                                                                         Length 4944;
                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hu ₩,
                                                                                                                                       Query Match
1.3%; Score 49; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus fumigatus essential gene #2372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-029590P.
09-UUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                  ABT20014 standard; DNA; 5362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2002; 2002WO-US013142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-093124/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                           ABT20014;
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                                                                                                                                                                                                                                                                                                                              RESULT 70
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New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or Idjands invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                     Sequence 5362 BP; 1321 A; 1343 C; 1334 G; 1364 T; 0 U; 0 Other;
                                                                                                                                                                                     Length 5362;
                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                     DB 7; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cervical cancer marker nucleic acid 638.
                                                                                                                                                                           1.3%; Scor.
100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berger A,
                                                                                                                                                                                                                                                                                                                                                                         AAH69364 standard; cDNA; 295 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000; 2000WO-US033312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0171350P.
2000US-0189315P.
2000US-0203791P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlegel R, Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200142467-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2001
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The invention relates to a purified nucleic acid molecule associated with cartation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second mucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX14836-ABX49947, or complements of them. Also included are complemented to a promoter and a 3 non-translated sequence that acid linked to a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of transcription and addition of polyadenylated ribonucleotides to a 3' end of transcription and addition of polyadenylated ribonucleotides to a 3' end of transcription and addition of the complementary nucleic acid sequences or its complementary nucleic acid molecule obtained from the bovine cell or tissue complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the complement and analyses, carried to genetically improving cattle. The present sequence was not shown in the specif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                              Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                              Bovine EST associated with lactation/muscle/fat deposition #6036.
Sequence 337 BP; 150 A; 35 C; 40 G; 112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 6036; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tao N,
                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1999; 99US-0115707P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-2001; 2001US-00960352.
                                                                                                                                                         ABX40871 standard; cDNA; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                                  20-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-110599/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos Taurus.
                                                                                                                                                                                                        ABX40871;
                                                                                                               RESULT 72
                                                                                                                                     ABX40871
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Gaps

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0; Indels

1.3%; Score 48; DB 4; Le 100.0%; Pred. No. 5.1e-07; :ive 0; Mismatches 0;

Conservative

Local Similarity nes 48; Conserv

Query Match Best Loca Matches

Length 295;

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypetide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for informance, in assessing biodiversities, or in identifying matations in foremaics, in assessing biodiversities, or in identifying matations responsible for genetic disorders and other traits. The nucleotide for corresponding to the recombinant production of for chromosome and gene mapping, in the recombinant production of protein, or in generating antishodies specific for it. The present sequence is useful for generating antishodies specific for it. The present sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly from USTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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                                                                                                                                                                                                                                                                                                                         88; sequencing by hybridisation; SBH; expressed sequence tag; BST;
mapping; biodiversity; genetic disorder.
                                Gaps
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                                                                                                 Length 337;
                                                                   Query Match
1.3%; Score 48; DB 7; Length 337
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 401 BP; 243 A; 47 C; 50 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 16319; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stache-Crain B,
                                                                                                                                                                                       ACH29107 standard; cDNA; 401 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                        Human adult spleen cDNA #126
                                                                                                                                                                                                                                                        13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LABAT I.
STACHE-CRAIN B.
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-615964/58.
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                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RT,
                                                                                                                                                                                                                         ACH29107;
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(LABA/)
(STAC/)
(DICK/)
(JONE/)
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                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                               genome
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                                                                                                                                                                                                                       Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker;
pharmacogenomic marker, gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 5; Le
Pred. No. 4.8e-07;
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100.0%; Pred. No. ...
                                                                                                                                                                                               Human prostate expression marker cDNA 44832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 8889; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monahan JE;
                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                         ABV44841 standard; cDNA; 404
                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2001; 2001WO-US005171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0255281P
                                                                                                                                                                    (first entry)
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                     WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                            6-MAR-2000;
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                                                                                                                                     ABV44841;
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AAI87343
ID AAI87
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AAI87343 standard; cDNA; 418 BP

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Gaps

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Ouery Match
1.3%; Score 48; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 48; Conservative 0; Mismatches 0;

Length 401;

AAI87343;

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodilatory activity and activity, insue growth factor activity, immunomodilatory activity and activity, insue growth factor activity, immunomodilatory activity and activity, influencediates and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, cytokine, cell proliferation; cell differentiation, gene therapy, vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                          Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory, cancer, leukaemia; nervous system disorders, arthritis, inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 7403; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 418 BP; 222 A; 43 C; 62 G; 91 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 48; DB 4; Le
100.0%; Pred. No. 4.8e-07;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 8603.
                                                                                      Human polynucleotide SEQ ID NO 7403.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                        26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                      06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAO07412
                                                                                                                                                                                                                            domo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
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Matches
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Length 418; 0; Indels

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or retarment of cancer, laukaemia, nervous system diagnosis, arthritis and inflammation. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jervical cancer; cytostatic; pre-malignant condition; gene therapy; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 419 BP; 174 A; 78 C; 86 G; 81 T; 0 U; 0 Other;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cervical cancer marker nucleic acid 2441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
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                                                                                                                                 26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                              rang YT, Liu C, Drmanac RT;
                                                                                                                                                                 28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Conservative
                                                                                                                                                                                                                                                                                 WPI; 2001-514838/56.
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                P-PSDB; AAO08612
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                                                                  W0200164835-A2
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                                                                                                  07-SEP-2001
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AAH71167
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                                                                                                   New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                  The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-mallgnant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, secreted protein, diagnosis, cytostatic, immunosuppressive,
antiHIV, antiinflammatory; nootropic; neuroprotective, antiallergic;
osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
immune disease; inflammation; blood disorder; tumour; ss.
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                         GA, Rosen CA, Ruben SM, Duan R, Moore PA, Wei Y, Ni J, Florence KA, Young PE, Brewer Endress GA, Ebner R, Olsen HS, Mucenski M;
                                                                                                                                                                                                                                                                 Length 546;
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                             Sequence 546 BP; 240 A; 92 C; 83 G; 130 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                 1.3%; Score 48; DB 4; Le
100.0%; Pred. No. 4.5e-07;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein gene 48 SEQ ID NO:58.
                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                          Berger A, Zhao X;
                                                                                                                                Claim 1; Page 512; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                AAA26393 standard; cDNA; 619 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0094657P.
98US-0095486P.
98US-0095454P.
98US-0095455P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
12-MAY-2000; 2000US-0203791P.
09-JUN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US017130
                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                          Schlegel R, Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-195282/17.
                                                                               WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsoulis GA, Rc
Lafleur D, Wei Y,
Soppet DR, Endress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY91498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200006698-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1998;
06-AUG-1998;
06-AUG-1998;
12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                     AAA26393;
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                             RESULT 78
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the polymucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in Examples of the activities are: cytostatic; antidiabetic; antiathaltergic, osteopathic; antiatharthriti; antibacterial; antidiabetic; antiatharthritic; antibacterial; antidiabetic; antiatharm; antipsoriatic; antiatharthritic; antibacterial; antidiabetic; cancellorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions are useful for preventing, treating or proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the polymucleotides. Specific uses are described for each of the polymucleotides. Based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumouris, neurodegenerative disorders, developmental abnormalities and foctal described, and focated disorders, solizophrenia, osteoporosis, atthritis, infections, AlDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, replicatory disorders, repriretying their binding patthers, The proteins are also useful for an focativitying their binding patthers, The proteins are also useful for an account in the avamplification of the preservatives. The proteins are also useful for an analysis of the interview.
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New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; L6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 48; DB
100.0%; Pred. No. 4.4
ative 0; Mismatches
                                                                                                                                            Claim 1; Page 405-406; 634pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AN Y.
HAMILTON C M.
PRICE J L.
RAINES T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002023281-A1.
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(RAIN/)
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gene therapy;

Human, cytokine, cell proliferation, cell differentiation, gene thy accine, poptide therapy, stem cell growth factor, haematopolesis, tissue growth factor, immunomodulatory, cancer; leukaemla; nervous system disorders, arthritis; inflammation, ss.

26-FEB-2001; 2001WO-US004927.

WO200164835-A2.

07-SEP-2001.

Homo sapiens.

28-FEB-2000; 2000US-00515126. 18-MAY-2000; 2000US-00577409.

Fang YT, Liu C, Drmanac RT;

HYSE-) HYSEQ INC.

WPI; 2001-514838/56. P-PSDB; AAC07777.

Human polynucleotide SEQ ID NO 7768.

06-NOV-2001 (first entry)

AA187708;

AAI87708 standard; cDNA; 903 BP

RESULT 80 AAI87708

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Query Match
Best Local Similarity 100.
Matches 48; Conservative
       MATHEW A V.
LEDFORD B L.
WOESSNER J P.
               HAAS W D.
GARCIA C A.
KRICKER M.
                       SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HURBAN P.
                             (ALLE/)
(HOFF/)
(HURB/)
                       (SLAT/
               (HAAS/
                           DAVI/
           LEDF/
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The invention relates to an Arabidopsis thaliana nucleic acid (I)

comprising a sequence capable of hybridising under stringent conditions

comprising a sequence capable of hybridising under stringent conditions

compared to a sequence selected from any one (1 99 sequences (ARNB99231),

given in the specification or its fragment. A polypeptide (II) encoded by

cycle of the specification or its fragment. A polypeptide (II) encoded by

II, a transgenic plant (III) comprising an exogenous nucleic acid, is

cycle of screening a candidate agent for its biological effect. (I) is

useful in identifying homologous or related genes, in producing

compositions that modulate the expression or function of its encoded

cycle of the manipulation of cells, particularly plant cells. (I) is also useful in

cycle ordered physiological pathways. (I) is also useful for the genetic

manipulation of cells, particularly plant cells. (I) is also useful in

cycle ordered physiological pathways. (I) is also useful in studying

cycle of the streamed agents are useful for screening of biologically active

cycle or programs to identify agents that mimic or enhance the action of tolerance

factors. Such agents are useful in improved methods of treating

cycle active active active active active action of tolerance

factors. Such agents that mimic or enhance the action of tolerance

factors. Such agents that mimic or enhance the action of tolerance

factors. Such agents that mimic or enhance the action of tolerance

factors. Such agents that mimic or enhance the action of tolerance

factors in thibiting production of a biosynthetic product in a plant.

CYCLIII is useful for identifying other mediators that may induce

cycle approximate to environmental stress. (I) is also useful action

cycle approximate to environmental stress. (I) active that may affect the biological in the study of genetic function and regulation.

CYCL all any affect the biological in a leavent one or gene products

construction of the callular metabolism and for screeni
                                                    Haas WD;
                                                                                                                                                                                                                                                                                                                                           New Arabidopsis thaliana nucleic acid for identifying homologous ge
producing compositions that modulate the expression or function of
encoded protein, and mapping functional regions of protein.
                                               JP, Haas
Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 865 BP; 231 A; 191 C; 152 G; 291 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 579; 49pp + Sequence Listing; English.
Hamilton CM, Price JL, Raines TM, A, Mathew AV, Ledford BL, Woessner M, Slater T, Davis XR, Allen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/sequence.html?DocID=999909770445
Gorlach J, An Y, Hamil
Rameaka JG, Page A, Ma
Garcia CA, Kricker M,
Hurban P;
                                                                                                                                                                                                                                                 WPI; 2002-403163/43.
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.

Claim 1; SEQ ID NO 7768; 1399pp + Sequence Listing; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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1.3%; Score 48; DB 4; L
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA93117 standard; cDNA; 1136 BP
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ID AAAS
XX
AC AAAS
XX
DT 12-5
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Score 48; DB 6; Le Pred. No. 4.1e-07;

1.3%;

100.0%; Prec. ...

40

"secreted protein"

/*tag= a /product= 135. .173 /*tag= b 174. .263 /*tag= c

Location/Qualifiers 93. .266

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Sequence 1136 BP; 351 A; 253 C; 249 G; 283 T; 0 U; 0 Other;
Human secreted protein coding sequence SEQ ID NO: 33.
                                                                                                                                                                                                                  Claim 42; Page 264; 309pp; English.
                                                                                                                                                                      Valenzuela D, Yuan O,
                                                                                                                                                             (ALPH-) ALPHAGENE INC
                                                                                                                                                                                WPI; 2000-549267/50.
                                                                                                                                                                                     P-PSDB; AAB23617
                                                                                   WO200049134-A1
                                                                                                       18-FEB-2000;
                                                                                                                    23-APR-1999;
17-AUG-1999;
23-SEP-1999;
01-OCT-1999;
29-NOV-1999;
                                                                                                                                                  15-FEB-2000;
                              Homo sapiens
                                                                                             24-AUG-2000
                                                                                                                 19-FEB-1999
                                                           sig_peptide
                                                                    mat_peptide
                                       Key
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99US-0167823P 2000US-0182711P

99US-0120680P. 99US-00298733. 99US-0149639P. 99US-0155686P. 99US-0167822P.

2000WO-US004340

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The invention relates to the isolation of genes AAC78997-C79045 encoding 49 human secreted proteins AAB44315-B44382. The genes can be used to generate faithin proteins by linking to the gene for the human compared to the gene for the human protein of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliocating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the conditions, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone constrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) marrow, breast, autoimmune thyroiditis, diabetes mellitus, crohn's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple scleromis, theumatoid arthritis and ulcerative collisis, (c) cardiovascular disorders such as myocardial ischaemias, (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fourty nine nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
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100.0%; Pred. No. 3.7e-07;
vative 0; Mismatches 0; Indels
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                                                               Human secreted protein gene 46 clone HPWAO89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 336-337; 367pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                      33-MAR-2000; 2000WO-US007725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1999; 99US-0126602P.
14-JAN-2000; 2000US-0176063P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-594640/56
P-PSDB; AAB44379.
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                                                                                                                                                                                                                                                             Homo sapiens
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ID ABK6
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AC ABK6
XX
DT 24-:
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the coding sequence for a human secreted protein. The sequence was isolated from an adult lung cDNA llbrary. The proteins and coding sequences of the invention can be used in the proteins similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have tases as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune autoimmune diseases, as haematopoiesis regulators (treating myeloid or lawbee chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-inflammatory activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted proteins and polynucleotides encoding them, which are derived from Homosapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements.
                                        Human; secreted protein; cytokine; cell proliferation;
nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rapiejko P;

Hoffman H, Hall J,

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DB 3; Le

1.3%; Score 48; DB 100.0%; Pred. No. 3.9 cive 0; Mismatches

Local Similarity 100. ses 48; Conservative

Matches

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Query Match

AAC79042 standard; DNA; 1467 BP

RESULT 82
AAC79042
ID AAC7
XX
AC AAC7

AAC79042

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The invention describes polypeptides and their salts containing the sequence of human N-Tes polypeptides or derived from it, and inhibiting the activity of membrane-type matrix metalloprocteinses. The polypeptides are used for the treatment, prevention and diagnosis of cancer and cancer infiltration, angiogenesis, Alzheimer's disease and arthritis, and especially of glioma. This sequence encodes the novel N-Tes polypeptide described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human N-Tes polypeptide and its partial sequences inhibiting matrix metalloproteinase for treatment and diagnosis of glioma and other neurological and neoplastic disorders.
                                        Human; N-Tes; membrane-type matrix metalloproteinase inhibitor; cancer; cancer infiltration; anglogeneals; Alzheimer's disease; arthritis; glioma; cytostatic; antiarthritic; nootropic; neuroprotective; antianglogenic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPP1 binding factor 1; MAP1; transgenic plant; chimeric gene; NMP1; nuclear matrix protein-1; FLIP; filament-like protein; transcriptional activator; protein composition; crop growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 48; DB 6; Length 1510; Local Similarity 100.0%; Pred. No. 3.7e-07; Less 48; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1510 BP; 507 A; 291 C; 335 G; 377 T; 0 U; 0 Other;
                                                                                                                                                                                /*tag= a
/product= "N-Tes"
/note= "Matrix metalloproteinase inhibitor"
            cDNA encoding matrix metalloproteinase inhibitor, N-Tes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding a filament-like protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 114-115; 129pp; Japanese.
                                                                                                                                                     socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA46483 standard; cDNA; 1544 BP
                                                                                                                                                                                                                                                                                                                                                                   (DAII-) DAIICHI FINE CHEM CO LTD
                                                                                                                                                                                                                                                                                                       27-DEC-2001; 2001WO-JP011529.
                                                                                                                                                                                                                                                                                                                                      27-DEC-2000; 2000JP-00398817.
                                                                                                                                                                  .1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crop protection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-538473/57.
                                                                                                                                                                                                                                                                                                                                                                                                Sato H, Aoki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU98506
                                                                                                                                                                                                                                            WO200257448-A1.
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                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                          25-JUL-2002
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Matches
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The present sequence encodes a filament-like protein 4 (FLIP4), which is used in the course of the invention. The specification describes a method whereby gene expression in a stably transformed transgent plant cell is regulated using a chimeric gene that encodes NMP1 (muclear matrix protein comprising a promoter linked to a DNA binding domain, a coding sequence or its complement, and a polyademylation sequence. The second gene comprises a promoter, a DNA binding domain, MMP1 or FLIP to polynucleotides, and a polyademylation sequence. Expression of the first gene regulates expression of the second. NMP1, FLIP and related proteins are parts of the methods are used to regulate gene expression in plants, comprises novel traits in transgenic plants that may result in new products useful in foods, pharmaceuticals and materials, or for products useful in foods, pharmaceuticals and materials, or for products useful in foods, pharmaceuticals and materials, or for suppression or l(MP1) or MP1-binding protein composition, and to derive new phenotypes beneficial for crop growth and development. NMP1, FLIP and related proteins are used to alter level of expression of MPP1 cubinding factor 1 (MPP1) or MPP1-binding proteins in plants that inhibit activity of MPP1- or MAP1-binding proteins in plants that inhibit activity of MPP1- or MAP1-binding proteins, which are potentially useful
                                                                                                                                                                                                                                                                                                                                                                   Regulating gene expression in plant cells, useful e.g. for expressing new traits, by introducing genes for transcriptional activators that interact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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100.0%; Pred. No. 3.7e-07;
vative 0; Mismatches 0; Indels
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Location/Qualifiers
2. 1021
/*teal/product "filament-like protein/product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding human PRO protein, Seq ID No 39.
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                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                with nuclear matrix proteins.
                                                                                                                                                                    99WO-US025993
                                                                                                                                                                                                        98US-00187999
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P-PSDB; AAY93406.
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                                                                                             WO200028054-A2
                                                                                                                                                                    04-NOV-1999;
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                                                                                                                                18-MAY-2000
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   Key
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Gaps

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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polypeptides. The sequences of the 122 PRO polypucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in perioyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating the proliferation of normal human blood, for stimulating the proliferation of normal human blood, for stimulating the proliferation of normal human blood, weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO protein coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
tumour necrosis factor-alpha; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 39; 359pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               2000US-0253646P.
2000WO-US032678.
2000US-00747259.
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2000WO-US023328.
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                                                                                                                         29-JUN-2001; 2001WO-US021066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
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P-PSDB; AAU83611.
                                                                WO200208288-A2.
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01-DEC-2000;
20-DEC-2000;
20-DEC-2000;
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                                 Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                     24-AUG-2000;
10-NOV-2000;
                                                                                              31-JAN-2002
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The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polymucleotides are useful for preparing a medicament useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of from recombinant cell culture or natural sources. ACA6681-ACA6696 from represent DNA sequence encoding the human PRO pulypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                          Human, PRO polypeptide, secreted and transmembrane protein;
anti-PRO antibody, diagnostic assay, gene expression, tumour, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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1.3%; Score 48; DB 7; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 48; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                         cDNA encoding human PRO polypeptide #20.
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                                                                                                                        ACA66860 standard; cDNA; 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-2000; 2000US-0220638P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2002; 2002US-00230163
                                                                                                                                                                                          23-JUN-2003 (first entry)
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                   US2003036635-A1.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2003.
                                                                                                                                                                                                                                                                                                  gene; ss.
                                                                                                                                                         ACA66860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor.
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RESULT 87 ACD68612

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Query Match 1.3%; Score 48; DB 6; Length 1837; Best Local Similarity 100.0%; Pred. No. 3.6e-07; Matches 48; Conservative 0; Mismatches 0; Indels

Gaps

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Indels

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Mismatches

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Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
                                                                  polypeptide
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Human, secreted and transmembrane protein, PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiatteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; atterial restenosis; hemmatoid arthritis; angina; mycardial infarction; thrombophiebliis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                   Novel human secreted and transmembrane protein PRO10111 cDNA
                                                 ACA68516 standard; cDNA; 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2000; 2000US-0220664P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                          25-JUN-2003 (first entry)
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, Gurney AL,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38-MAY-2003.
  48;
                                                                                                                                                                                                                                                                                                        ACA68516;
  Matches
                                                                                                                                                                                           RESULT 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide comprises are sequences having e.g. 4834, 2504 or 1759 bp fully defined in the comprises or polymelectides are useful concluded and the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polymelectides are useful cas pharmaceuticals, diagnostics, blosensors or bioreactors. These are comparing the prosecting tumours (e.g. lung tumour, oclon tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour) concluding the proliferation or differentiation of chondrocyte concluding the proliferation of pericyte cells, or for modulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or cortilage disorders (e.g. sports injuries or arthitis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases. The PRO polypeptides are useful markers, or for chromosome content as molecular weight markers, or for chromosome content in the sequence of these diseases. The PRO polypeptides are useful markers, or for chromosome content in gene therapy, particularly for replacing a defective content of the presence of themse secreted and transmenbrane PRO polyperides are useful man content and proven content of the presence of the presence of the presence of the presence of these diseases. The PRO genes may gener in gener therapy, particularly for replacing a defective contents and proven the proposes, or for contents and the presence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or wounds in a mammal.
                                                                                                                                                                                                                                             antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; pericyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; oclon tumour; breast tumour; prostate tumour; rectal tumour; arthritus, bone disorder; cartilage disorder; sports injury; arthritis; wound; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood
                                                                                                                                                                    Novel human secreted and transmembrane protein PRO10111 cDNA
                                                                                                                                                                                                                         secreted and transmembrane protein; PRO; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 39; 314pp; English.
        ACD68612 standard; cDNA; 1837 BP
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                  (first entry)
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C, Gurney AL,
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Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                  17-SEP-2003
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                                                          ACD68612
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Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

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                                                          The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endochelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated manular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, ungina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 48; DB 7; Le
100.0%; Pred. No. 3.6e-07;
:ive 0; Mismatches 0;
Claim 2; Fig 39; 314pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.3
Best Local Similarity 100.
Matches 48; Conservative
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Score 48; DB 7; Length 1837; Pred. No. 3.6e-07;

1.3%; S

Query Match Best Local Similarity

PRO; proliferation; gene; pericyte cell; TNF alpha; chondrocyte; blood; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast; ss.

(first entry)

06-NOV-2003

ABT44528;

Human PRO10111 CDNA

Goddard A, Godowski PJ; shan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard Smith V, Stephan JF,

Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-503301/47

P-PSDB; ABJ72375.

(GETH) GENENTECH INC

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

26-AUG-2002; 2002US-00227884

US2003027988-A1

Homo sapiens

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New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence

Claim 2; Fig 39; 324pp; English.

, Godowski PJ; Watanabe CK, Wood WI;

tumor in a mammal.

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The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TNF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation, the stimulation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO cDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.
                                                                                                                                                                                                                         TNF-alpha; blood; chondrocyte;
                                                                                                                                                                                                                           PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyt
differentiation; dermal fibroblast; tumour; gene therapy; gene;
Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME, Goddard A, Smith V, Stephan JF, W
                                                                      ABT44245
ID ABT44245 standard; cDNA; 1837 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 39; 315pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2002; 2002US-00230414.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-521818/49.
                                                                                                                                                                                          Human PRO10111 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABJ72247.
                                                                                                                                                                                                                                                                                                                                     US2003050448-A1
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                          06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2003
                                                                                                                                                                                                                                                                cytostatic.
                                                                                                                        ABT44245;
                                                     RESULT 89
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The invention relates to a novel isolated PRO protein encoding nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumour in a mammal. Furthermore, the molecules of the invention may be useful for stimulating pobliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNR)-alpha from human blood, the proliferation or differentiation of chondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO cDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, ss; chondrocyte stimulation; TNF-alpha stimulation; gene thuman dermal fibroblast stimulation; tumour; tissue typing; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane polypeptide PRO 10111 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. no.
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Pred. No.
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nes 48; Conservative
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affinity purification.

Homo sapiens

ABT44528 standard; cDNA; 1837

1729

RESULT 90 ABT44528 ID ABT4 XX

Query Match

Best Loca Matches

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Gaps

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Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

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The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate itemiliation, TNP-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents cDNA encoding a human secreted/transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human membrane bound receptor/protein PRO10111 cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .Match
Local Similarity 100.0%; Pred. No. 3.6e-07;
tes 48; Conservative 0; Mismatches 0;
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                                                                                                           28-AUG-2002; 2002US-00230338.
                                                                                                                                                     01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                     Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-492274/46.
                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABO34270.
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                         US2003044934-A1.
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                                                                 36-MAR-2003
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Matches
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A3743901
ID ABT43
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AC ABT43
DT 16-OC
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DE Human
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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate convironment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may be useful for the manmal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the cDNA sequence encoding a human PRO protein of the invention
                                                                                                                                                                                                                                                    PJ;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human, secreted and transmembrane protein, PRO; gene, ss; cytostatic, vulnerary, antiarthritic, pericyte cell proliferation, pericyte cell differentiation, chondrocyte cell proliferation, chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                           One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted and transmembrane protein PRO10111 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.3%; Score 48; DB 8; Length 1837;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB83529 standard; cDNA; 1837 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 39; 315pp; English.
                                                                                             24-FEB-2000; 2000WO-US005004.
02-WAR-2000; 2000WO-US005841.
01-UUN-2001; 2001WO-US017800.
29-UUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                    29-AUG-2002; 2002US-00232224
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                                                                                                                                                                                                                                                        Desnoyers L,
                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                 WPI; 2003-522018/49.
P-PSDB; ABJ72077.
                                                                                                                                                                                                                                                          Baker KP, De
Grimaldi JC,
                                                                            28-JUL-1999;
24-FEB-2000;
03-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                       tumor.
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Length 1837;

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WPI; 2003-644806/61
                             P-PSDB; ADB83530
                                                                                   PRO polypeptide.
         US2003073814-A1.
      Homo sapiens
           17-APR-2003
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ADB80635;
                                                                                                                                                                                                                                                    RESULT 94
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CD polypeptide (I) PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the pro116cration of or gene expression in
useful for stimulating the pro116cration of or gene expression in
cor stimulating PRO357, PRO325, PRO1306 or PRO1409 polypeptide
are useful for stimulating the release of tumour necrosis factor (TMF)-
alpha from human blood. PRO982, PRO317, PRO1725, PRO1306, PRO1419, PRO1414,
PRO1217, PRO1317, PRO1327, PRO1327, PRO1316, PRO1419, PRO1419,
PRO1227, PRO1317, PRO1327, PRO1318, PRO1419, PRO1419, PRO1419,
PRO1237, PRO1327, PRO1327, PRO1338, PRO1419, PRO1419, PRO1419,
PRO1237, PRO1347, PRO1366, PRO186, PRO1367, PRO1419, PRO14112,
PRO1248, PRO1367, PRO1367, PRO1367, PRO1419, PRO14112,
PRO1258, PRO1367, PRO1367, PRO1408, PRO1478, PRO1414, PRO14127,
PRO1378, PRO1367, PRO1367, PRO1408, PRO1478, PRO1414, PRO1413, PRO1414, PRO1413, PRO1414, PRO1413, PRO1414, PRO1418, PRO1418, PRO1418, PRO1414, PRO1418, PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; treast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3%; Score 48; DB 8; Length 1837; Best Local Similarity 100.0%; Pred. No. 3.6e-07; Matches 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
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Gaps ; 0

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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I) PRO982, PRO1160, PRO1137 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO237, PRO222, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO235, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (INF)-cr are useful for stimulating the release of tumour necrosis factor (INF)-cr pRO247, PRO337, PRO353, PRO1036, PRO1419, PRO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                               Human, secreted and transmembrane protein, PRO; gene, 88; cytostatic, vulnerary, antiarthritic; pericyte cell proliferation; pericyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; ummour necrosis factor alpha release; (TNF)-alpha release, dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour, breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
Novel human secreted and transmembrane protein PRO10111 cDNA.
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                                                                                                                                                       ADB80635 standard; cDNA; 1837
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09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-657982/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy.
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in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypepides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour prostate tumour, rectal tumour or typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO329, PRO1272 or PRO4405 polypepide is useful for treating bone and/or cartilage disorders (e.g., arthritis, proper injuries). This sequence encodes a human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                    PRO polypeptide.
                  88888888888888888
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Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

ö Gaps ö Length 1837; Score 48; DB 8; Length 105. Pred. No. 3.6e-07; Pred. No. 3.1 Indels Query Match Best Local Similarity 100.0%; Pred. No. 3.69

à 셤 ADB73176 standard; cDNA; 1837 BP.

ADB73176;

04-DEC-2003 (first entry)

vulnerary; antiarthritis; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) -alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; chondrocy; unmour; brast tumour; prostate human; secreted and transmembrane protein; PRO; gene; ss; cytostatic; Novel human secreted and transmembrane protein PRO10111 cDNA. gene therapy RESULT 95
ADB73176
ADB73176
ADB73177
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Homo sapiens.

US2003096968-A1.

22-MAY-2003.

29-AUG-2002; 2002US-00232223.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Desnoyers L, 2003-765525/72. Grimaldi JC, Baker KP,

P-PSDB; ADB73177.

New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating arthritis and tumors.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are Claim 2; Fig 39; 308pp; English.

useful for stimulating the proliferation of or gene expression in bericyte cells. PR0259, PR02192 or ER04405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PR0211, PR0357, PR0229, PR02155, PR03106 or PR04419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF).

The strong the proliferation or differentiation of chondrocyte care useful for stimulating the release of tumour necrosis factor (TNF).

PR0247, PR0313, PR0356, PR0363, PR0311, PR0183, PR03106, PR011019, PR01141, PR01134, PR01134, PR01134, PR01136, PR01137, PR01274, PR01137, PR011339, PR01137, PR01137, PR01137, PR01137, PR0 ô Gaps ö Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other; 1.3%; Score 48; DB 8; Le 100.0%; Pred. No. 3.6e-07; tive 0; Mismatches 0; Query Match
Best Local Similarity 100.0
Matches 48; Conservative PRO polypeptide. ð g

ADB78258 standard; cDNA; 1837 BP

(first entry) 04-DEC-2003

Novel human secreted and transmembrane protein PRO10111 cDNA.

vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; (TNF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; thundur; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; Human; secreted and transmembrane protein; PRO; gene; ss; cytostatic; gene therapy X#XBX#X#X#X#X#X#X#X#X

Homo sapiens

JS2003092889-A1

13-AUG-2002; 2002US-00219478

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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
           (GETH ) GENENTECH INC
               Baker KP,
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Company properties and isolated RPO (secreted and transmembrane)

Company peptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in percyce cells. PRO357, PRO125, PRO1305 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO355, PRO1355, PRO3306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMP).

Company PRO237, PRO982, PRO357, PRO355, PRO1306, PRO1419, PRO241, PRO31080, PRO1414, PRO337, PRO526, PRO1085, PRO330, PRO526, PRO1085, PRO330, PRO3414, PRO31080, PRO1414, PRO3130, PRO3414, PRO3130, PRO3414, PRO3130, PRO340, PRO3130, PRO3414, New isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers in protein electrophoresis, and for treating arthritis and tumors. Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; invention describes an isolated PRO (secreted and transmembrane) Claim 2; Fig 39; 308pp; English. WPI; 2003-765495/72. P-PSDB; ADB78259 PRO polypeptide.

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

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                          0; Indels
        1.3%; Score 48; DB 8; I 100.0%; Pred. No. 3.6e-07; tive 0; Mismatches 0;
Query Match
Best Local Similarity 100...
Local 8; Conservative
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ADB84906 standard; cDNA; 1837 ADB84906; RESULT 97
ADB84906
ID ADB8
XX
AC ADB8
XX
DT 04-D

(first entry) 04-DEC-2003

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polyunclectides encoding them.

Transmembrane polypeptides and the PRO polyunclectides encoding them.

The PRO polypeptides and polymuclectides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for prostate tumour, rectal tumour or liver tumour) in amammal, for prostate tumour cells, for the proliferation or differentiation of continulating the proliferation of or gene chood, for stimulating the proliferation of or gene commal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating continued and gene mapping, in generating technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therappetically useful reagents, in generating probes. The PRO polypeptides, or anti-PRO may be used in the development and screening of therappetically useful reagents, in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for creating and condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polymorpide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO polypeptides and nucleic acids encoding the polypeptides, usefule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                       transmembrane polypeptide;
                                       Human, PRO; gene, ss; secreted polypeptide; transmembrane polypeptid tumour, cancer; lung; colon; breast; protetter, rectum; liver; Lumour necrosis factor-alpha; TNF-alpha; blood; chondroyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
                                                                                                                          arthritis; sports injury; cytostatic; antiarthritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 39; 314pp; English.
                                                                                                                                                                                                                                                                                                                                           01-AUG-2000; 2000US-0222425P.
01-JUN-2001; 201NO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
Human PRO polymucleotide #20.
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C, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grimaldi JC,
                                                                                                                                                                         Homo sapiens.
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Gaps ö Length 1837; 0; Indels Score 48; DB 9; L Pred. No. 3.6e-07; 1.3%; Scc. 100.0%; Pred. No. 3.. ... 0; Mismatches Local Similarity 100.0 Query Match Matches

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

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RESULT 98 ADB78012

release;

tumour;

(first entry)

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

useful for stimulating the pro11feration of or gene expression in

pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

for stimulating the pro11feration or differentiation of chondrocyte

cells. PRO211, PRO125, PRO125, PRO1186, pPRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)-

alpha from human blood. PRO982, PRO1055, PRO1306, PRO1419, PRO1419,

PRO1478, PRO1314, PRO926, PRO1065, PRO1083, PRO10141, PRO1310,

PRO1286, PRO1181, PRO1186, PRO1186, PRO1187, PRO10137, PRO1274, PRO1310,

PRO1286, PRO1387, PRO1387, PRO1387, PRO1373, PRO1274, PRO13140,

PRO1286, PRO1387, PRO1387, PRO1380, PRO1414, PRO1317, PRO13140, PRO13186,

PRO1286, PRO1387, PRO1387, PRO1380, PRO1444, PRO13140, PRO1318,

PRO1286, PRO1387, PRO1387, PRO1380, PRO1414, PRO1317, PRO13140, PRO1322,

PRO1987, PRO1388, PRO1387, PRO1380, PRO1414, PRO1317, PRO13180,

PRO1987, PRO1388, PRO1387, PRO1380, PRO1414, PRO1317, PRO1418, PRO1818,

PRO1987, PRO1888, PRO1184, PRO1881, PRO1274, PRO4322,

CRO1481, PRO2229, PRO788, PRO1184, PRO1327, PRO1488, PRO4322,

PRO1881, PRO5225, PRO7154, or PRO1065 polypeptide are useful for checeting the presence of tumour in a mammal which

controles comparing the level of expression of the above PRO polypeptides

involves comparing the level of expression of the above PRO polypeptides

control eats sample of cells taxen from the mammal, and a control sample

control calls of the same cell type, where a higher level of expression of the indicative of the presence of tumour in the mammal call tumour is lung

the indicative of the presence of tumour in the temmular is lung

cumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour, rectal tumour, rectal tumour, rectal tumour or liver tumour, rectal tumour, rectal tumour, rectal tumour or liver tumour, rectal tumour or liver and propression of the prosence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated PRO polypeptide useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                     Human, secreted and transmembrane protein, PRO, gene, ss, cytostatic, vulnerary, antiarthritic; pericyte cell proliferation, chondrocyte cell differentiation, chondrocyte cell differentiation, tumour necrosis factor alpha release (TNR)-alpha release; dermal fibroblast cell proliferation, dermal fibroblast cell differentiation inhibitor; tumour, lung tumour; colon tumour, breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                          Novel human secreted and transmembrane protein PRO10111 cDNA,
ADB78012 standard; cDNA; 1837 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 39; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-2000; 2000US-0220607P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2002; 2002US-00216165.
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P-PSDB; ADB78013.
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                                                                                                                                                                                                                                                                                                                                                                                     gene therapy
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                                              ADB78012
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Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

Desnoyers L,

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typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO127 or PRO460 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This sequence encodes a human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMR)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PJ;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, PRO; gene, ss; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
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Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                              1.3%; Score 48; DB 9; Length 1837;
100.0%; Pred. No. 3.6e-07;
trive 0; Mismatches 0; Indels
                                                                                                                                                       Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polynucleotide #20.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity 100.0
Matches 48; Conservative
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Gurney AL,
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                                                                                                                       PRO polypeptide.
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Grimaldi JC,
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antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in issue typing. This sequence represents a human PRO polymucleotide of the invention.
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                                                                                                                                                                                                                                                                                              Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                 Score 48; DB 9; Le
Pred. No. 3.6e-07;
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Best Local Similarity 100.0%; Pred. No. 3.6
Matches 48; Conservative 0; Mismatches
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2000WO-US005004.
2000WO-US005841.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO polynucleotide #20.
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detecting tumours (e.g. lung tumour, colon tumour, breast tumour, corstate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) -alpha from human blood, for stimulating the proliferation of differentiation of conditions of conditions in periotyte cells, for stimulating the proliferation of or gene expression in periotyte cells or for stimulating the proliferation of or gene cormal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating anticonsome and gene mapping, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful cernology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful careparts and in generating tromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as periotyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for procein electrophoresis, and in tissue typing. This sequence represents a human PRO polymocial of the invention.
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Local Similarity 100.0%; Pred. No. 3.6e-07;
nes 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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Search completed: April 23, 2004, 04:26:38 Job time : 1354 secs.

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New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating arthritis and tumors.

Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard Smith V, Stephan JF,

Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC.

WPI; 2003-777259/73. P-PSDB; ADB84661. transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for

The invention relates to human PRO polypeptides (secreted and

Claim 2; Fig 39; 308pp; English.

us-10-005-907-1.oligo.rst

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AQ390121 CITRI-E1-
BR4431486 7022603.x
BR443113 6018604018
BZ600841 WHAAL89TR
BUID5429 AGBROCURT
AW668949 hi94 feb.x
A1766257 wh68904.x
BG445127 zw81b09.s
AQ006627 Zw81b09.s
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AQ006627 Zw81b09.s
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BR241033 601873444
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BR241034 GD0877341
AG182348 Pan trog1
BG7779208 MPL384 4
AG182348 Pan trog1
BG7779208 MPL384 8
BX370381 Baf6602
CR779208 MPL384 4
BX370381 Baf6602
CR779208 Jaf66106
CR779208 Jaf7661
CR779209 Jaf77609
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BU155309 AGENCOURT
BU171872 AGENCOURT
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CD639433 AGENCOURT
                                                                                                                        April 23, 2004, 04:04:06; Search time 8944 Seconds (without alignments) 12560.546 Million cell updates/sec
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                                                                                                                                                                                                                             Description
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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8

Searched:

Sequence:

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BFLG3 000 rj32f04.y UI-M-BZ1- BR230015A BX361013 rg79a01.y Mus muscu AGENCOURT	5', mRNA Sequence. ACCESSION BU155309 VERSION BU155309.1 GI:2266; KEYWORDS EST. GI:2266; SOURCE Home sapiens (human ORGANISM Home) sapiens Eukaryota; Metazoa;	Mammalia; Eutheria; Primates; Catarrhin; REFERENCE 1 (Dases 1 to 741) AUTHORS NIH-WGC http://mgc.nci.nih.gov/. TILE National Institutes of Health, Mammalian COMMENT Contact: Robert Strausberg. Ph. D.		Clone distribution: MGC clone distribution found through the I.M.A.G.E. Consortium/LLN http://image.llnl.gov Plate: LLCOM2350 row: n column: 08 High quality sequence stop: 512.	FEATURES Location Source 1.741 / vsgani	/db.xerf="texon:9606" /clone="IMAGE:6107719" /tissue type="from acu /lab host="HiloB (Tl pi /clone lib="NIH MGC 55	/note=Torgan: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: Sfil (ggcgcctcggcc); Site 2: Sfil (ggcTattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning follows: 5' and adaptor sequence: 5'-CACGGCCATTATGGCC-3' ar	3' adaptor sequence: 3'-ATTTAGAGGCGAGGCGGCGACGCGACTG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0,9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo	į	Query March Best Local Similarity 100.0%; Matches 665; Conservative 0	OY . 521 GAAACATTCCTTTCTGGCTAAAGTTTAGAAATATTATCTTATTATATATCCTTAGGCAAC	OY 581 TCTGATATGTGGCATCTCTGTGGCTTAGGTGAAATCATAGAAATTGACACAATGACCTAA 1	Qy 641 AATATTCTATGTGTTTTTGCTTGTAAAGTTTTGAGGACATGGAGGTGATAAAAAAACTTT 	Oy 701 CTTAGGACAATAATGTAAAATGAAAATTAAATTTCTAATCCCCCTGACTGA
B1376676 CD681869 BM938356 AW464287 BX361013 CF93621 BC049569 CK025580		BX326372 BX326372 BX369284 BX369284 BX369858 BX369858 BM459521 AGENCOURT BG25452 602568921 BG105078 602312365		CB409814 NISC nc07 B1496153 df123b08. CR299319 7LEAR03 CF595468 AGENCOURT A1611728 tw67h10.x	BG950530 PM0-CT070 AA420722 nc63b01.s CF316422 HD05-L0 BM773573 ra83e06.y	BF81447 MR2-C1018 CF31789 HD07-F1 BE906419 601498573 AA571130 VmC9C11.r CH04631 NISC GF07	CB977344 CAB40003_ BX056909 Single re AL698002 DKF2D686M BM155643 fv92009.y BM154953 fv91f07.y	CF804920 lad58e12. AA245921 mx06h06.r BM186145 fF98e03.y CA667403 wleul.pk0 AV949776 AV949776 AV949776 BW307133	BG111312 602283394 CD570788 kb76£12.y AW308314 3700 MARC	AW425882 58016 MAR CR621978 laf11c02. BIO44232 QV4-OT014 RHOG7075 FCR-1560	AL69799 DYFZD686M BU56667 AGENCOURT BI089903 602854962		AA562430 VK9BDD2.r BW212373 BW212373 BF080084 230839 MA BU155183 AGENCOURT	
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183 CTTAGGACAATAATGTAAAATGAAAATTAAATTTCTAATCCCCCTGACTAACTGAATGGAC 242
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11 (Dases 1 to 785)
11 (Marc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab_host="DHIOB (TI phage-resistant)"
/clone_lib="NHH MGC 55"
/note="Organ: bone marrow; Vector: pbNR-LIB (Clontech);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arro
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratorium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2351 row: j column: 05
High quality sequence stop: 550.
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/db_xref="taxon:9606"
/clone="IMAGE:6108004"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KEYWORDS
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Homo sapiens
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             NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) .

Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAATCAGTTTTACTCAAGTGTGATTATATACAAGAAAATGTAACCACTGTAAGGGTAGA 3328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTATAAGAATTTTGTCAAATGTATTCACCCATGTAGTCACCTCCTTATGAAGAGACAGA 3388
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100.0%; Pred. No. 1.5e-108;
cive 0; Mismatches 0; Indels (
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1. 728
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/mol_type="missass"
/db xref="taxxn:966"
/dlone="IMAGE:30414375"
/tissue_type="moled"
/lab host="Pooled"
/lab host="Pooled"
/lab host="Dild" | 1 phage-resistant)"
/clone lib="NIH MGC 191" site 1: Sfil (ggccattatggcc);
Site 2: Siti (ggcgcctcggcc): Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA and Ionomycin. S' adaptor sequence:
S'-CACGGCCATATAGGCC-3' and 3' adaptors sequence:
S'-CACGGCCATATAGGCC-3' and 3' adaptor sequence:
S'-CATTCTAGAGGCCGACATG-dT(30)BN-3' (where S'-ATTCTAGAGGCCGACATG-dT(30)BN-3' (where B = A, C, Or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                  CD639433 728 bp mRNA linear EST 17-JUN-2003
AGENCOURT 14532881 NIH MGC 191 Homo sapiens cDNA clone
IMAGE:30414375 5', mRNA sequence.
3569 TCATCTATGTTTAATGTTCTATCAGTAGTTGTACATCTTACTTGTCTCAGCATATCACCA 3628
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                                          543 TCATCTATGTTTAATGTTCTATCAGTAGTTGTACATCTTACTTGTCTCAGCATATCACCA 602
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NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Contract: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Selbesda, MD 20892

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: Narayan Bhar

CDNA Library Arrayan Bhar

CLONTECT CONSOrtium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDCM10 row: n column: 16

High quality sequence stop: 604.
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us-10-005-907-1.oligo.rst

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/clone="IMAGE:6617922"
/lab_host="DH10B (T1 phage-resistant)"
/clone llb="NIH MGC 82"
/note="Organ: testis, Vector: pDNR-LIB (Clontech); Site_1:
fincte="Organ: testis, Vector: pDNR-LIB (Clontech); Site_1:
Sfii (ggocgctcggct); Site_2: Sfii (ggccattatggcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCCT' and 3' adaptor sequence:
5'-ATTCTACAGGCCGACATG-GT(3) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
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Best Local Similarity 99.8%; Pred. No. 8.2e-104;
Matches 645; Conservative 0; Mismatches 1; Indels (
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/clone="IMAGE:3641981"
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                                                                   Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                     Unpublished (1997)
Other GSSs: CITBI-E1-2548B21.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research Genetics (info@resgen.com). BAC
Glones are available from Research Genetics (info@resgen.com). BAC
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                                                                                          Venter,J.C.
Mae of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
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Seg primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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CalTech Human BAC Library D"
         Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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Pred. No. 2e-96;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DN
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="2548B21"
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ilarity 99.7%;
Conservative 0
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-GAAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@mage.lln.gov
Seg primer: -40UP from Gibco
High quality sequence stop: 476.
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/clone_lib="NCI CGAP_Kidl1"
/note="Organ: Kidney; Vector: pr713D-Pac (Pharmacia) with
/note="Organ: Kidney; Vector: pr713D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: ECC RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and so circles were made in vitro. PolTowing HAP
purification, this DNA was used as tracer in a subtractive
hybridization. Tacation. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clone1Ds 1322376-1323911, 1456007-1456775, and
1500552-150285). Subtraction by Bento Soares and M.
Patima Bonaldo. "
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490
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                                                                                                      1403 ATATGTCCAAGAATCTTCAATTCCAAGCCTGCTCACCAAATTTCAAATGCCAACATCT 1460
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1 (Dases 1 to 549)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Dukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 757)

Yolik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Chin, K., Kuo, W.-L., Magrane, G., de Jöng, P., Gray, J.W. and Collins, C.

End-sequence profiling: Sequence-based analysis of aberrant genomes Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHAAJ89TR Human MCF7 breast cancer cell line library (MCF7_1) Homo Bapiens genomic clone MCF7_1-3010, genomic survey sequence.

BZ600841
inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ACTICIAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATT
                                                                                                                                                     0; Gaps
                                                                                                        Length 527;
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0; Indels
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Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
                                                                                                             DB 10;
                                                                                                             Query Match
13.5%; Score 506; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.4e-87;
Matches 506; Conservative 0; Mismatches 0;
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Email: svolik@cc.ucsf.edu
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E. 1 (Dases I to 527)

NH-MCC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM993 row: a column: 01

High quality sequence atop: 518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P242113 527 bp mRNA linear EST 14-NOV-2000 S1880401F1 NIH_MGC_55 Homo saplens cDNA clone IMAGE:4109064 5',
                                                                     TCCTTATGAAGAGACAGGTACATCCTCCCAGAAAGTTCCACAGTGCTCCTTTTCC 3430
                                                                                                                                                         3431 CTGAGTTTCACCAGTCCTGGCAACCAATGATCTGCTTTCGTATAATTATAACTGTTCTAGA 3490
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      369 TCCTTATGAAGAGACAGAACACGTACATCCTCCCAGAAAGTTCCACGGGCTCCTTTTCC
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/done="InAGS:619838"
/tissue_type="from acute myelogenous leukemia"
/lab host="nB108 (T1 phage-resistant)"
/lab lost="nB108 (T1 phage-resistant)"
/lone lib="NIH MGC 55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: Sfil (ggccgctcggcc); Site 2: Sfil (ggccattatggcc); Juble-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3/ adaptor sequence.
5/-ATTCTAGAGGCCGAGGCCGACATG-dT(30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3029 GGAACGIIGAAAICCAAGAGCAICAAIGICIICIGGIGGIICACCAIAAGCCACAGAGA 3088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2609 GITICAGAITITIGGAGCAITICAGAICITCAGAITAGGGAITITCAACCIGIACIGACCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 CIGTAGATATTAGCCAATTTTAGGAAAATGACAAAATTTTTTTACTTTTTCGTCTGCCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2669 TTTAGTCATTGACAAGCATTAATCAATAGGTGGACTCCAGATAACTCATTTGCTGTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 ACATTTTGCCTCTCTATTCAACGAATTCTTATGCCCTCTTGTGGTGATTTTAATGTGCGG
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                     CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2352 row, h column: 03
High quality sequence stop: 399.
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Pred. No. 1e-78;
0; Mismatches 1; Indels (
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       Fissue Procurement: ATCC
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99.8%;
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Best Local Similarity 99.8
Matches 512; Conservative
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                                                                                                                                                                                                                                        /clone lib="Human MCF7 breast cancer cell line library (MCF7])"
/note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
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11 (bases 1 to 786)
11 MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                12.5%; Score 471; DB 28; Length 757; 100.0%; Pred. No. 2.1e-80; tive 0; Mismatches 0; Indels
This clone is available from Amplicon Express
                                                                                                                      /organism="Homo sapiens"
mol_type="genomic DNA"
/db_xref="texon:9606"
/clone="MCP7]-3010"
/sex="female"
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                                                                         Location/Qualifiers
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                             http://www.genomex.com
Class: BAC ends.
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Homo sapiens
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3579 ITAATGITCIAICAGIAGITGIACAICITACITGICICAGCAIAICACCAIAIAGAIAIA
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AI766257/c
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/mol_type="mktA"
/db_rxef="taxon:9606"
/db_rxef="taxon:9606"
/db_rxef="taxon:9606"
/db_rxef="taxon:9606"
/dloxe="DH10B"
/dlost="DH10B"
/dlost="DH10B"
/dlost="DH10B"
/note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbH119W, testis NHT, and B-call NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302097, 682632-687239, 726408-728711, and 729096-731339. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                EST 06-APR-2000
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                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 504)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL , contact the
This Consortium (infc@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
Location/Qualifiers
1..504
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                                                S04 bp mRNA linear ES:
hi94£08.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2979975 3', mRNA sequence.
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                                           MRNA
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                        AW665849.1 GI:7458398
                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CAR clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1086 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 437.
Location/Qualifiers
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144 TIAATGTICTATCAGTAGTIGTACATCTTACTTGTCTCAGCATATCACCATATAGATATA 85
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| organism="Homo sapiens"
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| mol_type="mRNA" |
| db xref="taxon:9606" |
| cell line="HT1080" |
| cell line="HT1080" |
| follow="bathersys RAGE Library" |
| note="See Creation of Genome-wide Protein Expression |
| ibraries using Random Activation of Gene Expression |
| Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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BS461807.1 GI:13750313
BST.
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                                                                                              336 CCAGAAAGTTCCACAGAGTCCTCAATGATTTCACCAGTTTCACCAGTCCTGGCAACCAATGATC 277
                                                                                                                                                                                                                                                                                                                                                 TTTGTGTGTGTAAGGCTTCTTTTAGTCATTATAATATTTTTGAGATTCATCTATGTTAA 157
GTCAAATGTATTCACCCATGTAGTCACCTCCTTATGAAGAGACAGAACACGTACATCCTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 TGTTCTATCAGTAGTTGTACATCTTACTTGTCTCAGCATATCACCATATAGATATACTAT 97
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                                                             3403 CCAGAAAGTTCCACAGTGCTCCTTTTCCCTGAGTTTCACCAGTCCTGGCAACCAATGATC
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10.3%; Score 387; DB 12; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.1e-64;
Matches 387; Conservative 0; Mismatches 0; Indels 0
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Tel: 216 431 9900
Fax: 216 361 9596
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Location/Qualifiers
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Gaps

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/lab host="DH10B"
/clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac"(Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLML; contact the
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I (Bases I to 416)
Hillier, J., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Morce, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Wabhle, Y., Wylie, T., Waterston, R. and Wilson, R.
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                                                                          387 CTGTAAGGGTAGAGTTATAAGAATTTTGTCAAATGTATTCACCCATGTAGTCACCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                    3436 TITCACCAGICCTGGCAACCAATGAICTGCTITCGTATAAAITATAACTGTTCTAGATAITI
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 186)
Adams, M.D.; Rounsley, S.D.; Zhao, S.; Field, C.E.; Bass, S.; Linher, K.;
Golden, K.; Berry, K.; Granger, D.; Suh, E.; Wible, C.; Shizuya, H.;
Simon, M. and Venter, J.G. Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other GSSs: CIT-HSP-2294F11.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr.; Rockville, MD 20850, USA
Tel: 301 838 0200
Email: maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 bp DNA linear GSS 26-JUN-1998
GIT-HSP-2294FIL.TF CIT-HSP Homo sapiens genomic clone 2294FIL,
AQ006627
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                                                                                                                                                                                                            FICCCIGAGITICACCAGICCIGGCAACCAAIGAICIG 3464
                                                                                                                                                                                                                                                                              TGIGTGTGTAAGGCTTCTTTTAGTCATTATAATATTTTTTGAGATTCATCTATGTTTAATG 3584
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                                                                                                                                                                                                                                                                                                               223 IGIGIGIGIAAGGCTICTITIAGICATIAIAATATTITIGAGATICATCTATGTTAATG 164
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Seg primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 TTTGTTAATCTAATCACTGATGGATATGTAGGATATTTAAGTTTTTGACATTATGAATAA 44
                                                                                                                                                                                                                              343 AGAAAGITCCACAGAGTGCTCCTTTTCCCTGAGTTTCACCAGTCCTGGCAACCAATGATCTG
                                                                                                                                                                            0; Gaps
                                                                                                                                      Score 316; DB 9; Length 416;
Pred. No. 7.1e-51;
D; Mismatches 0; Indels
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/organism="Homo sapiens"
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                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pr
Matches 316; Conservative 0;
                                                                                                                                                                                                            3405 AGAAAGTTCCACAGTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3705 AGTGGCTATAAATGAA 3720
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Homo sapiens
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AQ006627/c
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/mol type="mrsm" or process
/mol type="mrsm" or process
/db xref="taxon:9606"
/clone="IMAGE:4091961"
/tissue type="from acute myelogenous leukemia"
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/clone lib="NIH MGC 55"
/note="Organ: Done marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil
ggcatatagacs); Double-stranded combA was prepared from cell line RNA. 5, and 3, adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF240893 809 bp mRNA linear EST 14-NOV-2000 601875444F2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091963 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          947 ACTCTGGTGTAGATCACACACTGTCTGAGGGATTCCATCTATGAGACTTTGTCTACATAA 1006
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(Dases 1 to 809)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM94B row: h column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            827 AGGIGAGACACCTIGITATACCCCTICCCTITIGGAGITTATGCACAAGTGACCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 AGGTGAGACACCTTGTTATACCCCTTCCCTTTTGGAGTTTATGCACAAGTGACCAGGA
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                                                                                                          /cell_type="Sperm"
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HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 CAGAGACCTITGCACAACCCCTITATITIAGCTAAAGCATICTITITGTA 82
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                                                                                                                                                                                                                                                                                         Length 386;
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100.0%; Pred. No. 3.6e-35;
ative 0; Mismatches 0;
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Location/Qualifiers
db_xref="GDB:7152159"
                  /db_xref="taxon:9606"
/clone="2294F11"
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Homo sapiens
                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 233; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 848)

1 (bases 1 to 848)

1 (bases 1 to 848)

2 NIH-MGC http://mgc.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

2 Unpublished (1959)

2 Contact: Robert Strausberg, Ph.D.

2 Email: Gapber Fremal.nih.gov

Trissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl.)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl. at:

http://mage.llnl.gov

Plate: LLCM984 row: c_column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 bp mRNA linear EST 14-NOV-2000 61877334F1 NIH_MGC_SS Homo sapiens cDNA clone IMAGE:4105665 5', BF243193
5'-ATTCTAGAGGCCGAGGCGGCGGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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436 AITICCACAACCCCTITITIAGCIAAAGCATICTITICTACIGACTICTIAAGICTIT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             958 GATCACACACTGTCTGAGGGATTCCATCTATGAGACTTTGTCTACATAACAGAGACCCTTG 1017
                                                                                                                                                                                                                                                                                                           777
                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         838 ACCTIGITATACCCCTTCCCTTTTGGAGTTTATGCACAAGTGACCAGGATGAGTCATAAG 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 ACCTIGITATACCCCTTCCC-TTGGAGTTTATGCACAAGTGACCAGGATGAGTCATAAG 315
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                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                      Query Match 5.2%; Score 194; DB 10; Length 809; Best Local Similarity 99.5%; Pred. No. 4e-28; Matches 364; Conservative 0; Mismatches 1; Indels 1
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Homo sapiens
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Eujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPC1-43
BLO end sequences of Library RPC1-43
BLO end sequences of Library RPC1-43
B. Chibama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC).
1-7-22 Suchiro-chou, Tsurum-ku, Yokohama, Sciences Center (GSC).
1-7-22 Suchiro-chou, Tsurum-ku, Yokohama, Sciences Center (GSC).
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NTH MGC 55"
/note="Organ: bone marrow, Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggogectoggec); Site_2: Sfil
(ggocattateggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor sequence: 5'-CACGCCATATGGCC-3' and 5'-ATTCTACAGGCCGACGACGACGAGGGCGACATG-dT(3)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo, Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3109 CTAGTITITCAGCAAAGCAGCATTIAAGAAATGTAACTATCTTATGTGGGTTATGAAGAAC 3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG182348 643 bp DNA linear GSS 09-JAN-2002
Pan troglodytes DNA, clone: RP43-055I01.TJ, genomic survey
sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%; Score 163; DB 10;
100.0%; Pred. No. 2.7e-22;
tive 0; Mismatches 0;
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/organism="Pan troglodytes"
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Pan troglodytes
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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AG182348.1 GI:16712028
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Best Local Similarity 100.0
Matches 163; Conservative
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AG182348
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AV706915
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CA301835
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//organism="Homo sapiens"
//organism="MRNA"
//organism=saxon:9606"
//olone="IMAGE:4806908"
//issue_type="adenocarcinoma"
//ib_host="DH108 (T1_phage-resistant)"
//olone=lib="NH1MGC_60"
//organ: prostate; Vector: pDNR-LIB (Clontech);
//oce="Organ: prostate; Vector: pDNR-LIB (Clontech);
//oce="Organ: prostate; Vector: pDNR-LIB (Clontech);
//oce="Organ: prostate; Vector: ponr-LiB (Clontech);
//oce="Organ: ponr-LiB (Clontech);
//oce="Organ: ponr-liB (Tib prostate);
//oce="Organ: ponr
                                                                                                                                                                                                                                                                                                                                                                           3190
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM/AG7 row: i column: 05
High quality sequence stop: 123.
Location/Qualifiers
Location/Qualifiers
Location/Canigna Home Canigna.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 712)
                                                                                                                                                                                                                                                                                                                                                                           3131 TITAAGAAATGTAACTATGTGGTTATGAAGAACAATAGAATCATTGCTGTATAAG
                                                                                                                                                                                                                                                                                                                                                                                                            NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                Gaps
/mol_type="genomic DNA"
/db_xref="texon:9598"
/clone="RP43-055101.TJ"
/sex="mall type="lymphocytes"
/cell_type="lymphocytes"
/cell_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                 Length 643;
                                                                                                                                                                                                                                                                                                                0; Indels
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Local Similarity 100.0%; Pred. No. 1.7e-06;
nes 80; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3191 TGCTTTTTAACCTGTAAATT 3210
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Best Local S:
Matches 80,
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Length 712;

1.4%; Score 53; DB 12; 100.0%; Pred. No. 0.19;

Query Match Best Local Similarity

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                                                                                                                                                                                                                        CA301835 344 bp mRNA linear EST 01-NOV-2002 taa08g10.y1 Hydra cDNA library Hydra magnipapillata cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (Dass) 1. (1) Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q., Blode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q., Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Martin, J., Hallider, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Ronko, I., Tsagareishvili, R., Washu Hydra EST Project Washu Hydra EST Project Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Library was constructed by H. Bode and B. Blumberg DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hydra magnipapillata"
//organism="MkNa"
//db itype="mkNa"
//db Aref="taxon:6085"
//lab_nost="DHSalpha"
//clone lib="Hydra cDNA library"
//note="Wydrocr: pSPORT6; Site 1: NotI; Site 2: Sall;
//ibraries prepared by Phil Wigge, Plant Molecular and
Libraries prepared by Phil Wigge, Plant Molecular and
collular Biology, Lab (Detley Weigel), The Salk Institute
for Biologyical Science, 10010 North Torrey Pines Road, La
Jolla, CA 92037."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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   1 GAGAAACCGAGICACIGIGAAAAGAIGGGAAAIITAICICCIGCGAAAACICAG
                                                                  42 gagaaaccgagrcacrgrgaaaaaargggaaarrarcrccrgcgaaaacrcag
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                                                                                                                                                                                                                                                                                                                                                                 CA301835.1 GI:24464894
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Hydra magnipapillata
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Hydridae, Hydra.
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Gaps

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EST 03-DEC-2002
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Generation of ESTs from mixed pig cDNA libraries

Generation of ESTs from mixed pig cDNA libraries

Controllished (2002)

Controllished Fouchyta

Center for Animal Functional Genomics, Department of Animal Science
/lab_host="DH10B"
/clone lib="MPD"
/clone lib="MPD"
/clone lib="MPD"
/note="Organ pooled; Vector: pSPORT1; Site_1: Not1;
Site_2: Sal1; Library made from pooled tissue from
adipose, adrenal gland, blood leukocytes, brain,
cartilage, eye, heart, intestine, kidney, liver, lump
lymph nodes, mammary gland, myogenic satellite cells,
ovary, pancreas, pituitary gland, placents, skin, spinal
cord, spleen, stomach, tendon, testes, uterus, and
vascular from various developmental and physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michigan State University
B215 Anthony Hall, East Lansing, MI 48824, USA
E1 157 355 8443
Fax: 517 432 9168
Email: suchytas@msu.edu
Single Pass sequencing. Bases called and alt-trimmed with phred
v0.0204425.c. Vector identified by cross_match with the -minscore
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="MpI"
/note="Organ: pooled, Vector: pSPORTI; Site_1: NotI;
Site_2: SalI; Library made from pooled tissue from adipose, adrenal gland, blood leukocytes, brain, cartilage, eye, heart, intestine, kidney, liver, lung lymph nodes, mammary gland, myogenic satellite cells, ovary, pancreas, pituitary gland, placenta, skin, spinal vascular from various developmental and physiological stages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA779205 32 bp mRNA linear EST 03-DEC-20
MPL384 g I20 MPL Sus scrofa cDNA clone pSPORT1 5', mRNA sequence.
CA779205
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 322)
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1.4%; Score 51; DB
Best Local Similarity 100.0%; Pred. No. 1;
Matches 51; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="pSPORT1"
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/dev_stage="pooled"
/lab_host="DH10B"
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CA779205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA780165 190 bp mRNA linear BST 03-DEC-2002
MPL384 4_H01 MPL Sus scrofa CDNA clone pSPORT1 5', mRNA sequence.
CA780165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Steven P. Suchyta
Center for Animal Functional Genomics, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.

    (bases 1 to 190)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michigan State University
Bast Lansing, MI 48824, USA
Tel: 517 355 9438
Fax: 517 432 9168
Email: suchytas@msu.edu
Email: suchytas@msu.edu
Single Pass sequencing. Bases called and alt-trimmed with phred
v0.0204425.c. Vector Identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="ADBBXCO8"
/tismue_type="Adrenal gland"
/dev stage="Addilt"
/lab_host="SOLR"
/clone_lib="ADB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
Xho!
                                                                                                                                                                     Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
               Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Ghom, Tu, Y., Jia, J., Fu, G., Ren, S., Homo sapiens cDNA ADB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 1.4%; Score 52; DB 9; Length 733; Local Similarity 100.0%; Pred. No. 0.29; es 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center for Animal Functional Genomics.
Generation of ESTs from mixed pig cDNA libraries
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                    Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pSPORT1"
/sex="Male and female"
/tissue_type="pooled"
/dev_stage="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sus scrofa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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  (bases 1 to 733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: T7
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Gaps

FEATURES

RESULT 24 BX512688 LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Fukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. B. (bases 1 to 649)

S. (bases 1 to 649)
S. NIH-MGC http://mgc.nci.nih.gov/.
S. NIH-MGC http://mgc.nci.nih.gov/.
D. Unpublished (1999)
L. Ontact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov/
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://inage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
          DQ571861
UI.M-FCO-byc-b-06-0-UI.rl NIH_BMAP_FCO Mus musculus cDNA clone
IMAGE:5716133 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The following repetitive elements were found in this cDNA sequence: 17-74, >POLY_A#Simple_repeat (matched compliment) Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:5716133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                           Mus musculus (house mouse)
                                                                                          BQ571861.1 GI:21475178
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Best Local Similarity
Matches 51; Conserv
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BX370381
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                                                                                                                                                   EST 25-JUN-2003
                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (2008 1 to 502)
Hell,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free from RZPD; contact RXPD (clone@rzpd.de) for further information. Seq primer: T7, Primer sequence: TAATACACTCACTATAGGG.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Mouse Uniqueset - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
Contact: Ina Rolfs
RZPD Ceutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD, INAGEPS2333:
RZPDLIB; I.M.A.G.B. CDNA Clone Collection;
Mouse Uniqueset - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-
bin/showib.pl.cgi/response?libNo-981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerveg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX512688
BX512688 Soares mouse 3NME12 5 Mus musculus CDNA clone IMAGE952F2335 ; IMAGE:763318, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 13; Length 502;
Pred. No. 0.65;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db xref="taxon:10090"
clone="IMAGp952F2335 ; IMAGE:763318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'tissue type="fetus"
dev stäge="12.5dpc total fetus"
lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Sco...
100.0%; Pre
                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                            BX512688.1 GI:32242549
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Best Local Similarity
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FEATURES

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mRNA linear EST 08-MAY-2003
COT 25-NORMALIZED Homo sapiens
mRNA sequence.
                                  ö
                                  Gaps
                                                               1.4%; Score 51; DB 13; Length 649;
100.0%; Pred. No. 0.51;
iive 0; Mismatches 0; Indels
                                                                                                                                                                     931 bp
BX370381 Homo sapiens HELA CELLS
CDNA Clone CSODK003YN10 5-PRIME,
BX370381 GI:30447935
                                                                                                                                                                                                                  ACCESSION
VERSION
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Matches

ઠ g RESULT

ORIGIN

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODC010YP24"
location/Qualifiers
                                              organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF328728.1 GI:33805694
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nes 50; Conservative
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CF328728/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / organism="HOMO sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NX1871156 Thome sapiens NEWGOLASTONA Linear EST 08-MAY-2003 EX387156 Home sapiens NEWGOLASTONA COT 25-NORMALIZED Home sapiens CDNA clone CSODCOlOYPE 5-PRIME, MENA sequence.
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Li W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cubm. libraries and normalization
Unpublished (2001)
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BP 191 91006 ZVRY cedex - France
Bmall: seqrefégenoscope.cns.fr, Web. : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3161.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSSAA004ZA04QPI&cluster=3161.r. Contact :
Feng Liang Email: fliang@lifete.ch.com UR. :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSSAA004ZA04QPI.
                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 BYRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5501.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CSOBAG044ZE08_CS04189_l&cluster=5501.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG044ZE08_CS04189_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 0.35;
tive 0; Mismatches 0; Indels
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BX387156.1 GI:30455496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domo sapiens (human)
                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoscope
                                                                                                                                                                                                                        Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
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Matches 51; Conserv
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DRIGIN

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CF328728

NACL--03-M07.gl Rice callus plasmid cDNA library (NACL) Oryza
Estiva cDNA clone NACL--03-M07, mRNA sequence.
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/dev stage="proliferated callus on 2N6 media for 30 days"
/dev stage="proliferated"
/lab_host="E.coll DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/clone_ivector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
Coryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 80)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H. Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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100.0%; Pred. No. 6.3;
tive 0; Mismatches 0; Indels
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Tel: 82 31 330 6193
Fax: 82 31 31 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                      Query Match 1.4%; Score 51; DB 13; Best Local Similarity 100.0%; Pred. No. 0.27; Matches 51; Conservative 0; Mismatches 0
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mol type="mRNA"
(Aultivar="NacAong"
/db xref="taxon:4550"
/clone="NACL--03-M07"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinne; Mus.

Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinne; Mus.

Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,

Wylie,T., Thelang,B., Bowers,Y., Gibbons,M., Ritter,B., Bennet,J.,

Ronko,I., Tasgareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,

Waterston,R. and Wilson,R.,

Waterston,R. and Milson,R.,

WashU Stem cell EST Project

WashIngton on Milson of Medicine

Library materials provided by: Stappenbeck Th.S. and Gordon J.I.

Library materials provided by: Stappenbeck Th.S. and Gordon J.I.

Library materials provided by: Stappenbeck Th.S. and Gordon J.I.

Library materials provided by: Stappenbeck Th.S. and covett M. DNA sequencing

by: Washington University Genome Sequencing Center For information

(ridwellegemetries.watel.edu)

Putative full length read

vector to vector length is

Seq primer: -40RP from Gibco.

ESS.

1.120
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Tidaes I to 146).

Mylie,T., Theising,B., Marra,M., Hillier,L., Pape,D., Martin,J., Mylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tangareishili,R., Belaygorod,L., Grow,A., Maguire,L., MashU Stem cell EST Project
Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett
WashU, Human Genetics Division
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                                           EST 12-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/db_xref="taxon:10090"
/tisbsue_type="small intestinal epithelial progenitors"
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laf76f02.yl SiEP Mus musculus cDNA 5', mRNA sequence.
CF929023
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Mus musculus (house mouse)
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                                                                                                          CF929023.1 GI:38276827
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RESULT 29
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Contact: Rose Tidwell
WashU Stem cell EST Project
WashIngton University School of Medicine
WashIngton University School of Medicine
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Original lib:1st strand of cDNA was synthesized with reverse
transcriptase and oligo(dT) beads, then cDNA was amplified by PCR
using modified SWART primers. The final cDNA was cloned in pAMP1
vector in annealing reaction with Uracil DNA Glycosylase (UDG).
Normalized by generating biotin labeled linear PCR using original
lib cut with Sal I as template, followed with Sau3A digest, and
hybridizing with ssDNA from original lib. RNA provided by Jeff
Gordon lab and library construction by Rose Tidwell and Mike
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/db xref="taxon:10090"
/lab host="bHsalpha"
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/note="Vector: pAMP!" lst strand of cDNA was synthesized
with reverse transcriptase and oligo(dT) beads, then CDNA
was amplified by PCR using modified SMART primers. The
final CDNA was cloned in pAMP! vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
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Lablee09.V1 Normalized Small intestinal epithelia progenitors Mus musculus CDNA 5', mRNA sequence.

CD645057
Washington University School of Medicine list strand of CDNA was synthesized with reverse transcriptase a clist strand of CDNA was synthesized with reverse transcriptase aclise (21) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by J. Gordon lab.
Putative full length read vector length is Seq primer: -40RP from Gibco.
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CF545723.1 GI:34893153
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progenitors cells from conventionally raised C57/Bl6 mice"
/lab host="XLI Blue MRF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF259903 11-AUG-2003 148 bp mRNA linear EST 11-AUG-2003 15941h07.yl Normalized colon epithelial progenitors cDNA library Mus musculus cDNA 5', mRNA sequence. CF259903
                                                                                         /mol_type="mRNA"
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Tidwell, R., Cilfton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Washu Stem cell EST Project
Unpublished (2002)
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Mashington University School of Medicine
Its strand of CDNA was synthesized with reverse transcriptase and
oliso (dr) beads, then CDNA was amplified by PCR using modified
SWART primers. The final CDNA was cloned in pAMP1 vector in
annealing reaction with Uracil DNA Glycosylase (UDG). Library
constructed by R. Tidwell Y. Stappenbeck and J.I. Gordon. Library
re-arrayed by R. Tidwell.
Directive full length read
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100.0%; Pred. No. 3.4;
tive 0; Mismatches 0; Indels
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Tidwell and Mike Lovett."
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/db xref="taxon:10090"
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Matches 50; Conservative
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Sed primer:
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CF259903
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Mus musculus (house mouse)

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I (bases 1 to 149)

St Tidwell, F., Cilfton, Marra, M., Hiller, L., Pape, D., Martin, J., Wyle, T., Theising, B. Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Wyle, T., Tragareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Washu, Stem cell EST Project

Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett

Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett

Washu, Human Genetics Division

Washington University School of Medicine

Ist Etrand of Canda was amplified by PCR using modified oligo (dT) beads, then CDNA was amplified by PCR using modified sonstructed by Y. Korshunova and M. Lovett. Library materials provided by J. Gordon lab.

Putative full length as ambound M. Lovett. Library materials between to vector length is Seq primer: -40RP from Gibco.

Seq primer: -40RP from Gibco.
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/mol type="mcNA"
/db xref="taxon:10090"
/tissue type="colon epithelia progenitor cells"
/lab host="HHSalpha"
/clone lib="colon epithelia progenitors cDNA"
/note="vector: pAMP1; 1st strand of cDNA was synthesized
with reverse transcriptase and oligo(dr) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF545723 12-5EP-2003
Lad99f06.yl Colon epithelia progenitore CDNA Mus musculus CDNA 5', mRNA sequence.
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Increa" Vector: pAMP1; 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then CDNA was amplified by PCR using modified SMAT primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library materials provided by T.S. Stappenbeck and J.I. Gordon. Library constructed by R. Tidwell Y.Korshunova, M. Lovett. Library was re-arrayed by R. Tidwell."
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                                                                                                                                                                                                                                                                                                                                       DB 14; Length 148; 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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RESULT 34 CF970419 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CB 1 (bases 1 to 158)

Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Ronko,I., Tangarafishvili,R., Belaygorod,L., Grow,A., Maguire,L., Materston,R. and Wilson,R.

Mashu Stem cell EST Project

Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
Washu; Human Genetics Division
Washington University School of Medicine
Mashington University School of Medicine
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For Information
on obtaining a clone please contact: Rose Tidwell
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                                                                                                                                                                                                                                                                                                                                                                                                           / Laber="mus musculus" / Mml type="mRNA" / Mml type="mRNA" / Mml type="mRNA" / Mml type="msmall intestinal epithelial progenitors" / Lis beet="Disabpa Ultra Max cells (Invitrogen)" / Clone lib="Sign" / Clone lib="Sign" / Mote="Vector: pAMP1; The library was synthesized with modified SMART primers with dUTP at the end. After modified SMART primers with dUTP at the end. After annealing."
Unpublished (2002)
Contact: Jeff Gardon and Mike Lovett
WashU, Human Genetics Division
WashU, Human Genetics Division
WashIngton University School of Medicine
Hishrary materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library amterials provided by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wistl.edu)
Putative full length read
vector to vector length is
Seq primer: -40RP from Gibco.
Location/Qualifiers
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/tissue_type="small intestinal epithelial progenitors"
/lab_host="Bhfsalpha" Ultra Max cells (Invitrogen)"
/clone_lib="SiEP"
/note="Vector: pAMP1; The library was synthesized with
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laf79al0.yl SiEP Mus musculus cDNA 5', mRNA sequence.
CF929504
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1.3%; Score 50; DB
Best Local Similarity 100.0%; Pred. No. 3.2
Matches 50; Conservative 0; Mismatches
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Mus musculus
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CF929504
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KEYWORDS
SOURCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases I to 156)

1 idwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tagagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., WashU Stem cell EST Project
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                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Bases I to. 15.2)
1 (Bases I to. 15.2)
1 (Jakell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J.,
Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J.,
Ronko, I., Tasgareishvili, R., Belaygorod, L., Grow, A., Maguire, L.,
Washy Stem cell EST Project
Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
//organism="Mus musculus"
//db Irye="mRNA"
//db Xref="tax=1.0090"
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/tish host="PHSalpha Ultra Max cells (Invitrogen)"
/clone_lib="SiEp"
/note="Vector: pAMP1; The library was synthesized with
modified SMART primers with dUTP at the end. After
treatment with UDG the CDNA was cloned in pAMP1 vector by
annealing."
                                                                                                                                                                                     EST 24-NOV-2003
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laccino6.yl SiEP Mus musculus cDNA 5', mRNA sequence.
CF382304
                                                                                                                                                                   CF970419 152 bp mRNA linear El
lag03a12.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
CP970419
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EST

REFERENCE AUTHORS

TITLE

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 35 CF382304

Query Match Best Local S

Matches

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Gaps

Query Match

Best Loca Matches

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 37 AW315672 LOCUS

REFERENCE AUTHORS

JOURNAL MEDLINE PUBMED COMMENT

TITLE

FEATURES

ORIGIN

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Estimate (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

I (bases 1 to 174)

I (bases 1 to 174)

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1 (bases I to 175)

Shoemaker, R., Kaim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Riteer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_trpm="mkNa"
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/tisue_type="small intestinal epithelial progenitors"
/lab_host="DHSalpha Ultra Max cells (Invitrogen)"
/clone_lib="SiEp"
/note="Vector: pAMP1; The library was synthesized with
modified SMART primers with dUTP at the end. After
treatment with UDG the cDNA was cloned in pAMP1 vector by
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Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshumova Y. and Lovett M. DNA sequencing
Dy: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
Putative full langth read
vector to vector length is
Seq primer: -40RP from Gibco.
Location/Qualifiers
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100.0%; Pred. No. 2.9;
iive 0; Mismatches 0; Indels
lab94b10.y1 SiEP Mus musculus cDNA 5', mRNA sequence
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                                       CF354150 GI:33959782
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Glycine max
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Contact: Smith TPL.

Contact: VS Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4350

Eax: 402 762 4390

Enail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred

VO.980904-e. Vector identified by cross_match with the -minscore 20

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modified SMART primers with dUTP at the end. After treatment with UDG the cDNA was cloned in pAMP1 vector by annealing."
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1 (bases 1 to 171)
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/mol_type="mRNA"
/db_xref="texon:9823"
/tissue_type="pooled"
/lab_host="pollob"
/clone_lib="MARC_2PIG"
/note=""Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue From testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wiee, T., Rohrer, G.A., Pertea, G., Sultana, R., Cuokenbush, J., and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
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100.0%; Pred. No. 2.9;
tive 0; Mismatches 0; Indels
                                                                                                                                                                           1.3%; Score 50; DB 14; Length 158;
larity 100.0%; Pred. No. 3.2;
Conservative 0; Mismatches 0; Indels
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13217 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW315672
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BACKWARD: GTTTTCCAGTCACGACG
Plate: 9 row: B column: 12.
Seq primer: ATTTAGGTGACATATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW315672.1 GI:6744928
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les 50; Conserv
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RESULT 38 CF354150 LOCUS

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Gaps

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Mus musculus (house mouse)

ENALYPORTATION (Musculus Enkaryporation)

ENKARYPORTATION (Musculus Enkaryporation)

ENKARYPORTATION (Musculus Enkaryporation)

I (bases 1 to 183)

St Tidwell, F., Cilifon, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Wylie, T., Tragareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Mashi, Stem cell EST Project

Unpublished (2002)

Contact. Jeff Gordon and Mike Lovett

Unpublished (2002)

Contact. Jeff Gordon and Mike Lovett

Mashi, Human Genetics Division

Mashington University School of Medicine

Ist Etrand of ColDA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by J. Gordon lab.

Phtative full length is Seq primer: -40RP from Gibco.

Seq primer: -40RP from Gibco.

Seq primer: -40RP from Gibco.
Waterston, R. and Wilson, R.
Washu Stem cell EST Project
Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
Washu, Human Genetics Division
Washu, Human Genetics Division
Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwellegenetics.wustl.edu)
Putarive full length read
vector to vector length is
Seq primer: -40RP from Gibco.
Seq primer: -40RP from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes="Vector: pAMP1; The library was synthesized with modified SMART primers with dUTP at the end. After treatment with UDG the cDNA was cloned in pAMP1 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:10090"
/tiseue_type="small intestinal epithelial progenitors"
/lab hose="bHSalpha Ultra Max cells (Invitrogen)"
/clone_lib="SiEP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; Pred. No. 2.7; Conservative 0; Mismatches 0; Indels
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Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareishvili, R., Belaygorod, L., Grow, A., Maguire, L.,
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                                                                                                                                                                                                                                                                                                                                                               information
                                                                                                                                                              Tel: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntaville, AL 35801 For further informs

call: (800)-533-4363 or contact: ccu@resgen.com web site:
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| Organism="Glycine max" |
| Amol type="maxNa" |
| Ab xref="taxon:3847" |
| Alone="SOYBEAN CLONE ID: Gm-c1072-4612" |
| Lissue type="seedlings induced for symptoms of SDS |
| Abden Death Syndrome |
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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(CF379915.1 GI:34323337
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1.3%; Score 50; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.resgen.com
Seg primer: -40RP from Gibco
High quality sequence stop: 169.
Location/Qualifiers
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Mus musculus
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CF379915 LOCUS DEFINITION

RESULT 40

ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

AUTHORS

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0; Gaps

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Query Match Best Local 9

DRIGIN

Matches

DEFINITION ACCESSION VERSION

RESULT 42 CF970587 LOCUS

ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Elkikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Muse.

CE 1 (bases 1 to 215)

Ry Tidwell, R., Cilfton, S., Marra, M., Hillier, L., Pape, D., Martin, J.,

Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J.,

Wole, T., Tasgareishvili, R., Belaygorod, L., Grow, A., Maguire, L.,

Ronko, I., Tasgareishvili, R.,

Machus Stem cell EST Project

Unpublished (2002)

And Wilson, Maguire, L.,

Mashington University School of Medicine

Mashington University School of Medicine

Ist strand of cDNA was synthesized with reverse transcriptase and oligo (dT) beads, then cDNA was amplified by PCR using modified sy Mashington University School of Medicine

Ist strand of cDNA was synthesized with reverse transcriptase and oligo (dT) beads, then cDNA was cloned in pAMPI vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y. Korshumova and M. Lovett. Library materials

Putative full length read vector length is

Seg primmer. - 40RP from Glbco

High muslity semisore atom: 215
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/note="Vector: pAMP1; ist strand of cDNA was synthesized
/note="vector: pAMP1; ist strand of cDNA was synthesized
/with reverse transcriptase and oligo(dT) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
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                                                                                                                                                                                                                                                                   CF425041 215 bp mRNA linear EST 03-SEP-2003
lad14d09.y1 Colon epithelia progenitors cDNA Mus musculus cDNA 5',
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100.0%; Pred. No. 2.3;
ive 0; Mismatches 0; Indels
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EST.
Mus musculus (house mouse)
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nes 50; Conservative
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CF352096
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JOURNAL
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1 (bases 1 to 208)
1 (bases 1 to 208)
1 (bases 1 to 208)
1 (bases 1 to 208)
1 (akell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Materston, R. and Wilson, R.

Mupublished (2002)
Contact: Jeff Gordon and Mike Lovett
Washugton University School of Medicine
Ist strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCK using modified SMART primers The final cDNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA Was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in sector Length read vector Length is Seq primer: -40RP from Gibco High quality sequence stop: 1 to an anneal Location Qualifiers

1 Location Qualifiers
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/mol_type="maxm".
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/note="vector: pAMP!, lst strand of cDNA was synthesized
/note="vector: pAMP!, lst strand of cDNA was synthesized
with reverse transcriptuse and oligo(dT) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP! vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
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                                                              /ado.most=_bnsdring.
//ado.most=_bnsdring.
//clone lib="Colon epithelia progenitors cDNA was synthesized
//note="Vector: pAMP1; 1st strand of cDNA was synthesized
with reverse transcriptase and oligo(dT) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y.Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.0%; Pred. No. 2.7; Similarity 100.0%; Pred. No. 2.7; Conservative 0; Mismatches 0; Indels
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Mus musculus
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Best Local Similarity 100.
Matches 50; Conservative
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Gaps

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source

FEATURES

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0; Gaps

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

PEATURES

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/clone lib="colon epithelia progenitors CDNA"
/clone lib="colon epithelia progenitors CDNA"
/clone lib="colon epithelia progenitors CDNA"
/clone lib="colon epithelia progenitors CDNA"
/clone lib="colon epithelia"
/clone in pampli ector in annealing
final CDNA was cloned in pampl vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y.Korshunova and M. Lovett. Library
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Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B., Bowers,Y., Glibbons,M., Ritter,E., Bennet,J., Ronko,I., Tagarelshyli,R., Belaygorod,L., Grow,A., Maguire,L., Waterston,R. and Wilson,R.
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lag52g08.yl Colon epithelia progenitors CDNA Mus musculus CDNA 5',
mRNA sequence.
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Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Nashington University School of Medicine
SMART primers on the final color was amplified by PCR using modified
SMART primers. The final color was amplified by PCR using modified
SMART primers. The final color was amplified by PCR using modified
SMART primers. The final color was a manaling reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library materials
provided by J. Gordon lab.
Putative full length read
vector to vector length is
Seq primer: 40RP from Gibco
High quality sequence stop: 249.
High quality sequence stop: 249.
                               No si sequence available.

This clone (DKEZp4341035) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcerzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/tissue_type="testis"
/dev stage="adult"
/dev stage="adult"
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/note="Vector: pSport1; Site_1: Sall"
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consortium of the German Genome Project.
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llarity 100.0%; Pred. No. 2.2
Conservative 0; Mismatches
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Matches 50; Conserv
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//mol_type="misserines"
//mol_type="misserines"
//lab_host="misserines"
//lab_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Jeff Gordon and Mike Lovett
WashU, Human Genetics Division
WashLy, Human Genetics Division
WashLy, Human Genetics Division
Strand of DNA was synthesized with reverse transcriptase and
oligo(dT) beads, then CDNA was amplified by PCR using modified
SMART primers. The final cDNA was cloned in pAMP1 vector in
annealing reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library materials
purative full length read
vector to vector length is
Seq primer: -40RP from Gibco.
Seq primer: -40RP from Gibco.
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DKFZp434L035_r1 434 (8ynonym: htes3) Homo sapiens cDNA clone
DKFZp434L035_5', mRNA sequence.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases I to 230)
1 (Dases I to 230)
1 (Dases I to 230)
1 (Pases I to
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 233)
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This is the 5' sequence of the clone insert
Clone from S. Witemann, Wolecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germann) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5433688.
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Local br. 50;

Matches

ALO45558 LOCUS DEFINITION

RESULT 45

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

JOURNAL

TITLE

REFERENCE AUTHORS

Query Match

ORIGIN

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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 47 CF805201

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259 bp mRNA linear EST 14-JUL-2000 ut07g01.yl Soares thymus 2NbMT Mus musculus cDNA clone IMAGE:3327216 5', mRNA sequence.
AW022602 255 bp mRNA linear EST 13-SEP-1999 df41b12.yl Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485966 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                    Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 255)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Buks musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         performed by National Institutes
Jenter (NISC; see
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
71el: 617 738 6396
Fax: 617 738 6396
Email: ccmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.nisc.nih.gov).
This clone is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LiAMG186 row: C column: 23 Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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1.3%; Score 50; DB 9; Length 255;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2485966"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE332081.1 GI:9205857
                                                                                                     AW022602.1 GI:5876132
                                                                                                                                                      Homo sapiens (human)
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VERSION
                                 DEFINITION
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PUBMED
COMMENT
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                                                                                ACCESSION
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Mus musculus
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi,
I (bases 1 to 250)
Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
Rylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
Ronko,I., Tasgareishvil,R., Belaygorod,L., Grow,A., Maguire,L.,
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
Onpublished (2002)
Contact: Jeff Gordon and Mike Lovett.
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                                                                                                                                                                                                                                                                                                                                                      CF605201 250 bp mRNA linear EST 24-OCT-2003
lad64c06.y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="dastric Epithelial Progenitor 2"
/cloce="Vector: pAMP1, 1st strand of cDNA was synthesized
/note="Vector: pAMP1, 1st strand of cDNA was synthesized
with reverse transcriptase and oligo(dT) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y.Korehunova and M. Lovett, Library
materials provided by Mills JC & Gordon JI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="Laser-captured isthmal cells from tox176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
Washington University School of Medicine
Ist strand of CDNA was synthesized with reverse transcriptase a
oligo(dT) beads, then cDNA was amplified by PCR using modified
SMART primers. The final cDNA was cloned in pAMP1 vector in
annealing reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library materials
provided by Mills JC & Gordon JI.
Putative full length read
vector to vector length is
Seq primer: -40RP from Gibco.
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                                                                                                                                                                                                                                 1.3%; Score 50; DB 14; Length 250;
100.0%; Pred. No. 2;
tive 0; Mismatches 0; Indels
                                                                                Length 249;
                                                                                                                                 Indels
            materials provided by J. Gordon lab."
                                                                                                                                 ö
                                                                                   14;
                                                                                1.3%; Score 50; DB
llarity 100.0%; Pred. No. 2;
Conservative 0; Mismatches
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db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransgenic mice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF805201.1 GI:37974603
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                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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                                                                                Query Match
Rest Local Similarity
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Gaps

Query Match Best Local Si Matches 50;

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ORIGIN

RESULT 48 AW022602

us-10-005-907-1.oligo.rst

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/note="Vector: pBluescript II XR, Site 1: EcoRI; Site 2: XhoI; This CDNA library was constructed from mRNA isolated from mmature flowers of field grown plants. The CDNA library was prepared using the Stratagene pBluescript II XR library construction Kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with ANOI restriction site. EcoRI adapters were ligated to the blunt-ended CDNA fragments followed by XhoI adgestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated CDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2 5).

Tidwall,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L., Watereton,R. and Wilson,R.

Masho, Stem cell EST Project
Unpublished (2002)
Contact: Rose Tidwell
WashU Stem cell EST Project
Unpublished (2002)
Contact: Rose Tidwell
WashU Stem cell EST Project
WashU Stem cell EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 280 1800
Fax: 314 280 bads, then cDNA was amplified by PCR
Using modified SWART primers. The final cDNA was cloned in pAMPI
vector in annealing reaction with Ureacil DNA was cloned in pAMPI
vector in annealing reaction with Ureacil DNA was digest, and
lib cut with Sal I as template, followed with Sau3A digest, and
                   Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 308 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD645268 261 bp mRNA linear EST 17-JUN-200
lab20h12.y1 Normalized Small intestinal epithelia progenitors Mus
musculus CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                /organism="Glycine max"
/mol type="mkNn"
/db Arzef="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-10682"
/tissue type="immature flowers of field grown plants"
/lab hose="KL10-Gold"
/clone_lib="Gm-c1016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 50; DB 10; Length 261;
100.0%; Pred. No. 1.9;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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Matches 50; Conserv
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COMMENT
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CD645268
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 261)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kudaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW/33655 261 bp mRNA linear EST 03-DEC-2001 8k83d01.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-10682 5', mRNA sequence.
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                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                 Tumor Gene Index (1997)
Contact: Robert Strausberg, Ph.D.
Email: Gapbbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.3%; Score 50; DB 10; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 50; Conservative 0; Mismatches 0; Indels
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Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol type="mxNA"
/strain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:3327216"
                                                                                                                                                                                                                                                            Seq primer: -40RP from Gibco
High quality sequence stop: 166.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="4 weeks"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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TITLE

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Gaps

EST 17-JUN-2003

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/clone="INAGE:2693416"
/tissue type='hapatic adenoma"
/lab host="MIDB"
/clone_lib="NCI_CGAP_Lis"
/note="forgan: liver; Vector: pCMV-SPORT4; Site_1: Sal1;
Site_2: NOt1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 0.8 kb."
                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 50; Conserv
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CF352983
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Email: cgapbs-remail.hih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI, send email to:

info@image.llnl.gov

Putative full length read
The vector to vector length is 337
Seq primer: -40RP from Gibeo.
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AMB27290
                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="small intestnal epithelial progenitor cells"
/lab_host="Xi." Blue MRF'"
/clone_lib="Normalized Small intestinal epithelia
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                hybridizing with ssDNA from original lib. RNA provided by Jeff
Gordon lab and library construction by Rose Tidwell and Mike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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100.0%; Pred. No. ...
0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                       'organism="Mus musculus"
                                                                                                                                                  vector to vector length is
Seg primer: -40RP from Glbco
High quality sequence stop: 261.
Location/Qualifiers
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126008.yl Colon epithelia progenitors cDNA Mus musculus cDNA 5', CT352983
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/clone_lb=Colon epithelia progenitors cDNA was synthesized
/note="Wector: pAMP1; 1st strand of cDNA was synthesized
was amplified by PCR using modified SWART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracii DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
                            ö
                            Gaps
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/mol_type="mRNA"
/db_xref="texcn:10090"
/tismue_type="colon epithelia progenitor cells"
/lab_hogt="DH5alpha"
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DB 10; Length 265;
                             0; Indels
                 1.9;
  ch 1.3%; Score 50; DB 1. Similarity 100.0%; Pred. No. 1.9 50; Conservative 0; Mismatches
                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                       CF352983.1 GI:33957496
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RESULT 54
CF380398
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

AUTHORS REFERENCE

TITLE JOURNAL COMMENT

FEATURES

ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases I to 294).

Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tasgaraishvili, R., Belaygorod, L., Grow, A., Maguire, L., Matsing Stem cell EST Project Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washly, Human Genetics Division
Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Stappenbeck Th.S. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustledu)
                                    Washu, Human Genetics Division
Mashu, Human Genetics Division
Mashington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
Dry Mashington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
Putative full length read
vector to vector length is
Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"

/db_xref="teaxon:10090"

/tissue_type="amall intestinal epithelial progenitors"

/lab_host="DH=small intestinal epithelial progenitors"

/lab_host="DH=small intra Max cells (Invitrogen)"

/clone_lib="SiEP"

/note="Vector: pAMP1; The library was synthesized with

modified SMAR! primers with dUTP at the end. After

treatment with UDG the cDNA was cloned in pAMP1 vector by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .294 | Most and the musculus | | /organism="Mus musculus | | /organism="Mus musculus | | /organism="Musu" | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= | /organism= 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF929133 294 bp mRNA linear B:
laf77h05.y1 SiEP Mus musculus CDNA 5', mRNA sequence.
CF929133
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Contact: Jeff Gordon and Mike Lovett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Mus musculus"
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vector to vector length is
Seq primer: -40RP from Gibco.
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Mus musculus
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CF929133
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Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Wash Ersten, R. and Wilson, R.
Wash Cstem cell EST Project
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washly, Human Genetics by solves of Washly, Human Genetics by solves of Washly, Human Genetics School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwall@genetics.whstl.edu)
Putative full length read
vector to vector length is
Seq primer: -40RP from Gibco.
Location/Qualifiers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 293)
Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tasagaraishvili,R., Belaygorod,L., Grow,A., Maguire,L., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
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/tissue_type="small intestinal epithelial progenitors"
/lab hose="misalpha Ultra Max cells (Invitrogen)"
/clone_lib="SiEP"
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Laccof08.y1 SiBP Mus musculus cDNa 5', mRNA sequence.
                                                                                                                                                                                                                         CF380398 293 bp mRNA linear E
lac46f08.yl SiEP Mus musculus cDNA 5', mRNA sequence.
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Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

DEFINITION RESULT 55 CF380717 LOCUS

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EST 12-NOV-2003

Query Match

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Best Loca Matches

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

DEFINITION

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RESULT 57 CF384267

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Musuccutus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (Dases I to 314)

I (Dases I to 10 14)

I (Inten), Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theiaing, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Wylie, T., Theiaing, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Washu Stem cell EST Project

Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett
Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett
Washington University School of Medicine
Nashington University School of Medicine
Ist strand of conk, was synthesized with reverse transcriptase and oligo (dT) beads, then CDNA was amplified by PCR using modified SNART primers. The final CDNA was aloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was closed in pampi provided by V. Korshunova and M. Lovett. Library materials
Putative full length read
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                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamaalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No all sequence available.

No all sequence available.

This clone (DKEZp4340045) is available at the RZPD in Berlin.

Please contact the RZED: Ressourcementum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Ingelstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKP2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="434 (synonym: hte83)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                             Wiemann, S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5433743.
Contact: MIPS
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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 50; Conservative 0; Mismatches
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/db_xref="taxon:9606"
/clone="DKFZp4340045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
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Mus musculus
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           Homo sapiens (human)
Homo sapiens
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/ Organism="Mus musculus"
//mol_type="mRNA"
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/lab_host="DH5alpha Ultra Max cells (Invitrogen)"
/lab_host="DH5alpha Ultra Max cells (Invitrogen)"
/lote="Vector: pAMP1; The library was synthesized with modified SMART primers with dUTP at the end. After treatment with UDG the cDNA was cloned in pAMP1 vector by annealing."
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Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Fighe,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L., Wasterston,R. and Wilson,R.
Washu Stem cell EST Project
Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
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Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library materials provided by: Korshunova Y. and Lovett M. DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Rose Tidwell
treatment with UDG the CDNA was cloned in pAMP1 vector by annealing."
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ALO45620.2 GI:5936045
EST.
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                                                                                                                                                                                                                                                                                        CF384267 301 bp mRNA linear E.
lac04h02.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
CF384267
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Local Similarity 100.0%; Pred. No. 1.7;
les 50; Conservative 0; Mismatches 0; Indels
                                                                                                                            Length 294;
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1.7;
                                                                                                                         Match 13%; Score 50; DB Local Similarity 100.0%; Pred. No. 1.7 es 50; Conservative 0; Mismatches
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Putative full length read
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RESULT 58 ALO45620 LOCUS DEFINITION

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Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tasqareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Wabh Stem cell EST Project
Unpublished (2002).
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Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on Obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
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/db xref="teaxon:10090"

/tissue_type="small intestinal epithelial progenitors"

/lab host="DHSalpha Ultra Max cells (Invitrogen)"

/clone_lib="SiEP"

/note="Yoector: pAMP1; The library was synthesized with

modified SNAR! primers with dUTP at the end. After

treatment with UDG the cDNA was cloned in pAMP1 vector by
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WashU Stem cell EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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laa83g11.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
CD422638
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100.0%; Pred. No. 1.6;
cive 0; Mismatches 0; Indels
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                                                                    organism="Mus musculus"
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Seg primer: -40RP from Gibco
High quality sequence stop: 321
Location/Qualifiers
                  Seq primer: -40RP from Gibco.
Location/Qualifiers
 vector to vector length is
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tes 50; Conservative
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CD422638
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AUTHORS
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                                  FEATURES
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SJEBDOOZ SJE Schistosoma japonicum cDNA, mRNA sequence.
BU767819
BU767819.1 GI:28335135
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

I (Bases I to 329)
Norio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Willame, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development
DNA Res 5 (6), 335-340 (1998)
                                                                                                                                                                                                                                                                                        AU034841 ST 28-APR-1999 MENA linear EST 28-APR-1999 AU034841 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLE570, MENA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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/clone_lib="blctyostelium discoideum SL (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schistosoma japonicum
Schistosoma japonicum
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hideko Urushihara
Institute of Biological Sciences
Institute of Biological Sciences
Institute of Biological Sciences
Inversity of Taukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-664
Email: hidekoghiol:tenkuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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                                                                                                                                                    ch 1.3%; Score 50; DB 14; Length 321; Similarity 100.0%; Pred. No. 1.6; 50; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 50; DB 9;
100.0%; Pred. No. 1.5;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:44689"
/clone="SLE570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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us-10-005-907-1.oligo.rst

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1...35)
/vrganism="Plasmodium falciparum 3D7"
/mol_type="mRNA"
/mol_type="mRNA"
/db_tref="mRNA"
/lab_host="mRNA"
/lab_host="mRNA"
/lab_host="mH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/note="Vector: pBluescript SK plus, Site_1: EooRi, Site_2:
Xhol; Library was constructed by Debopam Chakrabarti.
Xhol; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.18'-1ysed P. falciparum 3D7 infected
erythrocytes by the acidic quanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Fromega, WI) using streptavidin
Magnesphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (Smg)
into EcoRI and Xhol sites of 1 ZaplI vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the ExAssist helper phage
(Stratagene), the phagemids were precitptated with PBG
8000 and extracted with phenol/chloroform. Phagemid DNA
was electroporated into DH10B cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                  350 bp mRNA linear EST 29-MAY-2002 falciparum 3D7 asexual cDNA Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum 3D7 con 5', mRNA sequence.
BQ450975
BQ450975.1 GI:21254087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 350)
Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D., Barra,M., Hillier,L., Martin,J., Wylle,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,B., Bennett,J., Jentes,E., Ronko,I., Tsagareishvill,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Waterston,R., Wilson,R. and Sibley,D. Franklin,C., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: esr@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco.
Location/Qualifiers
/note="Vector: pAMP1; The library was synthesized with modified SMART primers with dUTP at the end. After treatment with UDG the cDNA was cloned in pAMP1 vector annealing."
                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contract: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                1.3%; Score 50; DB 14; Length 346;
100.0%; Pred. No. 1.5;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                   50; Conservative
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Fax: 314 286 1810
                                                                                                                                                                                                     Similarity
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Matches 5
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COMMENT
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BQ450975
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.
CB (bases 1 to 346)
RS 1'dwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
Ronko,I., Tasising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
Ronko,I., Tasagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
Washu Stem cell EST Project
AL Umpublished (2002)
Contact: Jeff Gordon and Mike Lovett
Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For Information
on obtaining a clone please contact: Rose Tidwell
Futative full length read
                              Hu, W., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R., Wang, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J., Ku, X.N., Wang, Z.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J., McManus, D.P., Xue, C.L., Feng, Z., Chen, Z. and Han, Z.G. Brolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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                                                                                                                                                                                                                                                     Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Shoujang Ruda, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
1911 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttissue type="small intestinal epithelial progenitors"
/lab host="DHSalpha Ultra Max cells (Invitrogen)"
Colone lib="61EP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF382593 346 bp mRNA linear Et
Lac88g07.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .336
/organism="Schistosoma japonicum"
/mol type="mRNA"
/db_Xref="taxon:6182"
/tissue_type="whole egg"
/dev stage="egg"
/lab_host="rabbits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
1.3%; Score 50; DB 13
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 50; Conservative 0; Mismatches

    .346
    /organism="Mus musculus"
/mol_type="mRNA"
    /db_xref="taxon:10090"

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Seg primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF382593.1 GI:34326017
         (bases 1 to 336)
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AUTHORS
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LOCUS
      REFERENCE
                                    AUTHORS
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

LOCUS DEFINITION

ACCESSION

RESULT 65 BE048163

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Single pass sequencing. Bases called and alt trimmed with phred v0.9809044.e. Vector identified by cross_match with the -minscore 18 pcR PRimarch 12 options.
FORWARD: AGGARACAGCTATGACCAT
               Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona, Phlebobranchia, Cionidae, Ciona.

1 (bases 1 to 366)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. I (bases 1 to 387)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J., Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="heart"
/clone_lib="Nori Satoh unpublished cDNA library, heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 50; DB 13; Length 366; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG895855 387 bp mRNA linear 359509 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEA: 402 762 4390
                                                                                                                                                                                                                                                                                                                         Email: satch@ascidian.zool.kyoto-u.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ciona intestinalis"
                                                                                                                                                                                                                                               Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
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1. .387
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciht012005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 124 row: I column: 6
Seg primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9823"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG895855
BG895855.1 GI:14306096
                                                                                                                                                                        Contact: Nori Satch
Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (pig)
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AUTHORS
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BG895855
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I Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: Gasbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Woll-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BW306217

BW306217 Nori Satoh unpublished cDNA library, heart Ciona intestinalis cDNA clone ciht012005 5', mRNA sequence.
                                                                                                                                                                                                                                                  BE048163 354 bp mRNA linear EST 08-JUN-2000 tz46g05.yl NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291672 5', mRNA sequence.
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/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
/clone_lib="NH108"
/clone_lib="NH2 CGAP_BEN52"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; This library represents the normalized version of NCI GAP_BEN15. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1:19 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblascoma, astrocytoma (grade II), medulloblascoma, astrocytoma (grade by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                               0; Gaps
                                                                            Query Match 1.3%; Score 50; DB 10; Length 354; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 50; Conservative 0; Mismatches 0; Indels
                               0; Indels
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 50; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 354
/organism="Homo sapiens"
/mol type="mRNA"
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Ciona intestinalis
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BW306217
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VERSION KEYWORDS SOURCE

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EST 05-JUN-2001

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1 (Dases 1 to 395)

WCCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dane, M., Marra, M., Hiller, L., Kuchabar, T., Theising, B., Wylie, T., Dane, M., Ritter, E., Bennett, J., Franklin, C., Teagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steproe, M., Allen, M., Person, B., Swaller, T., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel. 314 286 1810

Exx: 314 286 1810

Exx: 314 286 1810

Email: est@watson.wustl.edu
Cloned unidirectionally. Poly (A) + RNA was concentrated and purified using with oligo(GT) with Xho! Site (primer Coloned unidirectionally. Poly (A) + RNA was concentrated and primed with oligo(GT) with Xho! Site (primer CDSIII/3-xho!) and 5' SWART anchor added using chimeric DNA-RNA oligo (SWART-Noti-r-GGG). SMART-Noti-r-GGG was used in case a pcR using 1st strand and primers specific to SL1 leader sequence (SL1-Not!) and 5' SWART anchor added using chemically competent using lst strand and primer specific to SL1 leader sequence (SL1-Not!) fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM -11zf(+) plasmid. Chemically competent cells were used as host. This library was digested by David Bird but deaved be bott. Then library was digested by David Bird but deaved by David bird but deaved by David Bird, Putative full length read
The vector to vector length is 396
Seg primer: SGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 bp mRNA linear EST 25-NOV-2003 rg78c04.y1 Meloidogyne hapla female SL1 pGEM Meloidogyne hapla cDNA CF979559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Heteroderidae, Meloidogyninae, Meloidogyne.
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Site_2: Not1; Cloned unidirectionally. Poly_(A)+ RNA was
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/clone lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Libzary made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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                                                                                                                                                                                                                                                                                                       1.3%; Score 50; DB 12; Length 387; 100.0%; Pred. No. 1.3; Ative 0; Mismatches 0; Indels
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity 100.0
Matches 50; Conservative
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Meloidogyne hapla
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Theor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: Oavid B. Krizman, Ph.D.
CDNA Library Preparation: NG-CGAP clone distribution information can be found through the I.M.A.G.B. Consortum/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 601 Std Error: 0.00
Seg primer: -40ml3 fwd. ET Error: 0.00
Seg primer: -40ml3 fwd. ET Error: 0.00
Location/Qualifiers
concentrated and purified using Dynabeads (Dynal) and mRNA eluted for 1ST strand synthesis. 1st strand cDNA created using wmLV RT(PowerScript, Clontech) and primed with oligo (dT) with XhoI site (primer CDSIII/3-XhoI) and 5' SWART anchor added using chimeric DNA-RNA oligo (SWART anchor added using chimeric DNA-RNA oligo (SWART-NotIr-GGG). SWART-NotIr-GGG was used in case a PCR using the SWART template was also desired. 15 PCR cycles were done using 1st strand and primers specific to SLI leader sequence (SLI-NotI) and 3' end (XhoI-No-dT). dscDNA was digested using XhoII/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGBM -11zf(+) plasmid. Chemically competent cells were used as host. This library was provided by David Bird's lab (david bird@ncsu.edu), of North Carolina State
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="NCI_CGAP_Thyl"
/note="Vector: pAMP10; mRNA made from invasive thyroid
tumor, CDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert size
600 bp. Reference: Krizman et al. (1996) Cancer Research
56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA493109
19-AUG-1997
ng96e02.sl NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:942650
similar to contains element L1 repetitive element ;, mRNA sequence.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 407)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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db_xref="taxon:9606"
/clone="IMAGE:94250"
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Homo sapiens
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1.3%; Score 50; DB 9; Length 407;

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50; Conservative
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Meloidogyne hapla
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Best Local Similarity
Matches 50; Conserva
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Mus musculus

Mus pularia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Euthoria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 440)

1 (bases 1 to 440)

1 (thousing 10, Marra, M., Hillier, L., Pape, D., Martin, J.,

Mylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J.,

Ronko, J., Tsagareishvili, R., Belaygorod, L., Grow, A., Maguire, L.,

Mashu Stem cell EST Project

Unpublished (2002)
                                                                                                                                                                              AI133559 427 bp mRNA linear EST 11-NOV-1999
HA2177 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 427)
                                                                                                                                                                                                                                                                                                                                                                      Yu,Y., Zhang,C., Luo,L., Ouyang,S., Li,W., Wu,J., Zhou,S., Liu,M. and He,F.
                                                                                                                                                                                                                                                                                                                                                                                                Expression profile analysis of a human fetal liver cDNA library Unpublished (1998)
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/mol_type="mRNA"
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/tissue_type="liver"
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/lab_nost=="MC1061/p3"
/lab_nost=="Human fetal liver cDNA library"
/note="Vector: pCDNA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 427;
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                         Indels
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Department of Hematology
Bejing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
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1.3%; Score 50; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 50; Conservative 0; Mismatches
         Pred. No. 1.2;
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Contact: Jeff Gordon and Mike Lovett
100.0%; Prec. ...
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Location/Qualifiers
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                                                                                                                                                                                                                                AIÍ33559
AII33559.1 GI:6360875
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                                                                                                                                                                                                                                                                                Homo sapiens (human)
Homo sapiens
       Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                 sequence.
                                                                                                                                        RESULT 70
AI133559
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CF621874
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Hashington University School of Pedicine

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/lab.host="mlatle"
/lab.host="mlatle"
/clone_lib="Meloidogyne hapla female SL1 pGEM"
/clone_lib="Meloidogyne hapla female SL1 pGEM"
/clone_lib="Meloidogyne hapla female SL1 pGEM"
/clone_lib="Meloidogyne hapla female SL1 pGEM"
/clone_lib="Meloidogyne lib"
/ site_l: XhoI;
/cloned unidirectionally. Poly (A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for IST strand synthesis. lst strand cDNA created using of primer CDSIII/3-XhoI) and 5/
SMART anchor added using chimeric DNA-RNA oligo
/SMART anchor added using lst strand and primers specific to
SL1 leader sequence (SL1-NotI) and 3' end (XhoI-No-dT).
/dscDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested
DGEM -llf(+) plasmid. Chemically competent cells were
used as host. This library was provided by David Bird's
luhiversity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM958905 443 bp mRNA linear EST 18-MAR-2002 PLATE_11_C09_05.AB1 GS Lambda-Triplex, 10 day germinating spore library Glomus intraradices cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
using the SMART template was also desired. 15 PCR cycles were done using 1st strand and primers specific to SLA leader sequence (SLI-Norl) and 3' end (Xho-No-AT). dscDNA was disgested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM -11zf(+) plasmid. Chemically competent cells were used as host. This library was provided by David Bird's lab (david bird@ncsu.edu), of North Carolina State University. Seq primer: Sp6 High quality sequence stop: 441.
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Box 30001, MSC 3MLS Horseshoe Drive Las Cruces, NM 88003, USA Tel: 505-646-3918
Fax: 505-646-684
Email: plammers@nmsu.edu.
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Glomus intraradices
Glomus intraradices
Glomus intraradices
Glomus intraradices
Intraradices
Interaction Glomeromycota; Glomeromycetes; Glomerales;
Glomeraceae; Glomus.
Interaction to 443)
Bago, B., Zipfel, W., Williams, R.M., Jun, J., Arreola, R.,
Immmers, P.J., Pfeffer, P.E. and Shachar-Hill, Y.
Translocation and utilization of fungal storage lipid in the arbuscular mycorrhizal symbiosis
Plant Physiol. 128 (1), 108-124 (2002)
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                                                                                                                                                                                                                                                                                                      1. .441
/organism="Meloidogyne hapla"
/mol_type="mRNA"
/db_xref="taxon:6305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 1.3%; Score 50; DB 14
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 50; Conservative 0; Mismatches
                                                                                                                                                                                                                                                quality sequence stop: 441,
Location/Qualifiers
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BM958905.1 GI:19542335
                                                                                                                                                                                                                                                                                                                                                                                                                             sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Peter Lammers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
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COMMENT
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BM958905
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MEDLINE
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/notes "Vector: Lambda Triplex2; Site 1: SfiIA, Site 2: SfiIB; Spores were germinated in the presence of 1% CO2. At 10 days, tissue was ground in liquid nitrogen with sand and mRNA isolated with a modified hot phenol/SbS method. The SWART-PCR method (Clontech) was used for cDNA synthesis from 1 ug of total RNA followed by directional cloning in Sfil digested Triplex2 vector. Plasmid subclones in priplex were recovered by cre-lox excision in B. coli strain BM25.8 and sequenced from the 5' end with the 5'Triplex sequencing primer (Tpx) and the 3' end with the T7 primer (T7). (Sfil by in Comment line of EST file is estimated insert size)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C91260 C91260 Dictyostellum discoideum SS (H.Urushihara) Dictyostellum discoideum cBNA clone SSJ516, mRNA sequence.
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Dictyostellum discoideum
Dictyostellum discoideum
Eukaryota, Mycetozoa; Dictyostellida; Dictyostellum.
Eukaryota, Mycetozoa; Dictyostellida; Dictyostellum.
I (bases 1 to 457)
Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. Developmental CDM, in Dictyostellum discoideum
Unpublished (1998)
Contact: Hideko Urushihara
Institute of Biological Sciences
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                                                               /mol_type="mRNA"

db_xref="taxon:4876"

/tissue_type="germinating spore tissue"

fac_type="10 and after germination"

/ab_host="E. coli BM 25.8"

/clone_lib="GS Lambda-Triplex, 10 day germinating spore
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/clone="858J516"
/dev_stage="slug"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 50; DB 12; Length 443; larity 100.0%; Pred. No. 1.1; Conservative 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="AX4"
                                             organism="Glomus intraradices"
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Tsukuba
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JOURNAL
COMMENT
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C91260
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AUTHORS
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JOURNAL
COMMENT
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CB524236
LOCUS
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AUTHORS
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                                                                                           EST 09-OCT-2000
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Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wyle,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tsagareishvill,R., Belaygorod,L., Grow,A., Maguire,L., Waterston,R. and Wilson,R. WashU Stem cell BST Project
Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone_lib="ADB"
'note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Sis Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                           Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Shong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z. Homo sapiens CDNA ADB clones
Unpublished (2000)
                                                                                         AV707816 ADB Homo sapiens cDNA clone ADBECD06 5', mRNA sequence.
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100.0%; Pred. No. 1.1;
tive 0; Mismatches
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/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                   AV707816.1 GI:10725081
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                                                                                                                                                                                     Homo sapiens (human)
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CF546023
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Matches 50; Conserval
                                                                                                                                                                                                           Homo sapiens
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 408
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CF546023
LOCUS
DEFINITION
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AUTHORS
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JOURNAL
COMMENT
                                                     RESULT 75
AV707816
LOCUS
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AUTHORS
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EST.

Mus musculus (house mouse)

SM mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

SI (Dases 1 to 477)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gappbs-Fomail.nih.gov

Tissue Procurement: Dr. Jim.Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at Clone Distribution: Distribution information can be found at Clone Distribution: Distribution information can be found at Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Distribution information can be found at Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Distribution information can be found at Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Dr. M. Bonto Soares, University of Iowa Clone Distribution: Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soares Dr. M. Bonto Soare
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/mol type="mcNa"
/db_xref="taxon:10090"
/tissue_type="mcNa"
/db_xref="taxon:10090"
/tissue_type="colon epithelia progenitor cells"
/lab host="hHSalpha"
/lore="Vector: pAMP1; ist strand of cDNA was synthesized
/note="Vector: pAMP1; ist strand of cDNA was synthesized
/note="vector: pAMP1; ist strand of cDNA was synthesized
/note="vector: pAMP1; ist strand of cDNA was amplified by PCR using modified SNART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshunova and M. Lovett. Library
materials provided by J. Gordon lab."
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UI-M-GKO-cew-1-22-0-UI.rl NIH_BMAP_GKO Mus musculus cDNA clone
IMAGE:6846599 5', mRNA sequence.
WashU, Human Genetics Division
Mashington University School of Medicine
1st strand of CDNA was synthesized with reverse transcriptase and
1st strand of CDNA was synthesized with reverse transcriptase and
oligo(dT) beads, then CDNA was amplified by PCR using modified
SMART primers. The final CDNA was cloned in pAMP1 vector in
annealing reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y.Korshunova and M. Lovett. Library materials
provided by J. Gordon lab.
Putative full length read
vector Inength is
Seq primer: -40RP from Gibco
High quality sequence stop: 341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%; Score 50; DB 14 Best Local Similarity 100.0%; Pred. No. 1.1; Matches 50; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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High quality sequence stop: 503
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VERSION
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SOURCE
ORGANISM
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CD681869
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                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
/tissue_trype="Whole brain"
/dev stage="1, 5, and 15 days newborn"
/dab_bost="Whole (Ti phage resistant)"
/clone lib="NIH BMAP GKO"
/note="Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not! and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGANCTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 smc oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the amphicxus project site at: http://www.molgen.mpg.de/amphicxus/clones and filters are distributed via the Resource Center/Primary PCR PRimers
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483 bp mRNA linear EST 26-AUG-2003
BFLG3_000479 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG
or MPMGp498) Branchiostoma floridae cDNA clone MPMGp498B0638 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Panopoulou G
Laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innebtr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1128
Fax: +49 30 8413 1128
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J.,
Panopoulou, G., Hennig, S., Groth, D., Krause, A., Volugron, M. and Lehrach, H.
New evidence for genome-wide duplications at the origin of
Vertebrates using an amphioxus gene set and completed animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 50; DB 14; Length 477; Similarity 100.0%; Pred. No. 1.1; 50; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 13 (6A), 1056-1066 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    program coordinator."
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BI376676.1 GI:30911635
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Best Local Simi
Matches 50;
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BI376676
LOCUS
DEFINITION
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VERSION
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PUBMED
COMMENT
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/tissue_type="whole embryo"
/dev stage="5-6 hrs (gastula stage)"
/lab_host="E.coli, XLI blue"
/lab_host="E.coli, XLI blue"
/clone_lib="amphioxus 5-6 hrs cDNA library (Name
convention: BFLG or MPMGp489"
/note="Vector: pSport1; Site 1: Sall, Kpni, EcoRI (5');
Site_2: Not1, BamHI, HindIII (3'); OligodT primed and
directionally cloned in pSport1 vector using a Not1
(5'-pGACTAGTTGTAGATGCGAGGGGCGCC (T)15:3' and a Sall 5'-
TCGACCACGCGTCCG-3'adapters (Gibco BRL)."
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Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
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Wordarter, J., Califton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tragazatsishvili, R., Ronko, I., Kennedy, S., Maguirer, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu

The library was constructed by Claire Murphy and Dr. Makedonka
Dautova at Washington University. St. Louis
(mdautova@watson.wustl.edu). Oligo(dT).Stl Fased library.
Meloidogyne chitwoodi egg cDNA PCR products of size >400
mucleotides containing Stl on the 5' end and oligo(dT) on the 3'
end were non-direction ally cloned into pCRII-TOPO(Invitrogen)
following the Topo TA cloning protocol. Eggs were provided by Dr.
David Bird of North Carolina State University, Raleigh, NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD681869
503 bp mRNA linear EST 24-JUN-
rj3zE04-yl Meloidogyne chitwoodi egg ELI JODO vl Meloidogyne
chitwoodi cDNA 5' similar to SW:ELI35 CAEEL P34662 PROBABLE 60S
RIBOSOWAL PROTEIN L35. [1] ;, mRNA sequence.
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The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fat: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
INSert Length: 1200 Std Exror: 0.00
Seq primer: 5'-CGGTCCGGATTCCCGGGT-3' pSport3/86
High quality sequence stop: 483.
Location/Qualifiers
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1;
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                                                                                                                                                                                                                                                         /organism="Branchiostoma floridae"
/mol type="mRNA"
/db zref="taxon:7739"
/clone="MPMGp499B0638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.3%; Score 50; DB
Best Local Similarity 100.0%; Pred. No. 1;
Matches 50; Conservative 0; Mismatches
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meloidogyne chitwoodi
Meloidogyne chitwoodi
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0; Gaps

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562 bp mRNA linear EST 24-FEB-2000
BP230015A20F2 Soares normalized bovine placenta Bos taurus cDNA
Clone BP230015A20F2 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 217 333 5998

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uluc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

Research Initiative, Momack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trimmi g:

Cross match from Washington University Genome Center PHRAP suite.

Sequences submitted are vector free and at least 200 bp in length.
/clone lib="NIH BMAP MHI2_S1"
/note="Vector: pTyTab-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco R1; The NIH BMAP MHI2 S1 library is a subtracted library derived from NIH BMAP MHI2. NIH BMAP MHI2 is a library derived from NIH BMAP MHI2. NIH BMAP MHI2 is a library derived of the library from which this clone was derailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab.host="DHIOB"
/lab.host="DHIOB"
/clone_lib="Soares normalized bovine placenta"
/clone_lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pT773Pac; Site 1: EcoRI;
Site 2: NotI; The CDNA library was contributed by the
Soares aboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lewin, H. A. W. Reck Center for Contact on all Genomics W. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, Il
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 562)
Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and
                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 12; Length 515;
Pred. No. 0.98;
                                                                                                                                                                                                                                                                                                                0; Indels
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BACKWARD: ATTAACCCTCACTAAAG
INSERT Length: 562 Std Brror: 0.00
Plate: BP230015A20 row: F column: 2
Seg primer: ACGGAPTAACATTTCACACAGGA
High quality sequence stop: 562.
Location/Qualifiers
                                                                                                                                                                                                                                              1.3%; Scc. 100.0%; Pred. No. c. 0; Mismatches
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| Organism="Bos taurus"
| Mol_type="mENA"
| db xref="taxon:9913"
| Clone="BP230015A20F2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW464287.1 GI:7034455
                                                                                                                                                                                                                                                                                                             50; Conservative
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (cow)
                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
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COMMENT
                                                                                                                                                                                                                                                                                                                   Matches
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AW464287
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AUTHORS
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                                                                                                                              /dev_stage="eggs"
/lab_hote="MHIOB"
/clone lib="Meloidogyne chitwoodi egg SL1 TOPO v1"
/clone lib="Meloidogyne chitwoodi egg SL1 TOPO v1"
/clone lib="Meloidogyne chitwoodi sgt site_1: EcoR1;
Site_2: EcoR1; The library was constructed by Claire
Murphy and Dr. Makedonka Dautova at Nashington University,
St. Louis. Oligo(dT)-SL1 PCR based library. Meloidogyne
chitwoodi egg cDNA PCR products of size >400 nucleotides
containing SL1 on the 5' end and oligo(dT) on the 3' end
were non-directionally cloned into pCRII-TOPO(Invitrogen)
following the Topo TA cloning protocol. Eggs were provided
by Dr. David Bird of North Carolina State University,
Raleigh, NC (david_bird@ncsu.edu)."
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UI-M-BZ1-bfw-o-15-0-UI.rl NIH BMAP_MH12_S1 Mus musculus cDNA clone
UI.M-BZ1-bfw-o-15-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Mental Health
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
TTel: 301 443 1706
Fax: 301 443 8990
Email: mESTGmail.nih.gov
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 515)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 503;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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clone="UI-"+B2I-bfw-o-15-0-UI"
ddev stage="27-32 days"
lab_host="DH10B (Life Technologies)"
                                                         'organism="Meloidogyne chitwoodi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 50; DB
100.0%; Pred. No. 1;
Ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
97044477
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                                                               /mol_type="mRNA"
/db_xref="taxon:59747"
/dev_stage="n="-".
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          Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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es 50; Conserv
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/clone lib="mailtimed hapla female SL1 pGEM"
/note="Vector: pGEM-11zf(+) (Promega); Site_1: XhoI;
Site_2: NorI; Cloned unidirectionally. Poly (A)+ RNA was
site_2: NorI; Cloned unidirectionally. Poly (A)+ RNA was
concentrated and purified using Dynabeads (Dynal) and mRNA
eluted for 1ST strand synthesis. 1st strand cDNA created
using mALV RTPOwerScript, Clontech) and primed with
oligo(dT) with XhoI site (primer CDSIII/3-KhoI) and S'
SWART anchor added using chimeric DNA-RNA oligo
(SWART norIr-rGGG). SWART-NorIr-rGGG was used in case a
PCR using the SWART template was also desired. 15 PCR
cycles were done using 1st strand and primers specific to
SL1 leader sequence (SL1-NorI) and 3' and (KNOI-Nor-GT).
dscDNA was digested using XhoI/NorI; fractionated on
Chroma-spin 400 columns (Clontech) and ligated to digested
pGEM -11zf(+) plasmid. Chemically competent cells were
used as host. This library was provided by David Bird's
lab (david birdencsu.edu), of North Carolina State
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Cloned unidirectionally. Poly (A) + RNA was concentrated and
cloned unidirectionally. Poly (A) + RNA was concentrated and
cloned unidirectionally. Poly (B) + RNA was concentrated and
purified using Dynabeads (Dynal) and mRNA eluted for 1ST strand
synthesis. 1st strand cDNA created using MMLV RT(PowerScript,
CLonecch) and primed with oligo(dT) with Xhol site (primer
CDSIII/3.Xhol ) and 5' SWART anchor added using chimeric DNA-RNA
oligo (SWART-NotI-r-GGG). SWART-NotI-r-GGG was used in case a PCR
using 1st strand and primers specific to Sil leader sequence
(Sil-NotI) fractionated on Chroma-spin (Gschaw was digested using
Xhol/NotI, fractionated on Chroma-spin 400 columns (Clontech) and
ligated to digested pGEM -11zf(+) plasmid. Chemically competent
cells were used as host. This library was provided by David Bird's
lab (david birdenceu.edu), of North Carolina State University.
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Mus musculus, RIKEN CDNA 1700054013 gene, clone IMAGE:6772969,
                    McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagareishvil, R., Konko, I., Kennedy, S., Magnire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R., and Wilson, R., 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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/organism="Meloidogyne hapla"
/mol-type="mRNA"
/db xrefe="texon:6305"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="whole organism"
'dev_stage="adult"
|lab_host="DH108"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7394.f For
more information about this cluster, sequence cluster 7394.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI078CG100Pl&cluster=7394.f. Contact :
Feng Liang Email : fliang@lifetech.com URL:
Feng Liang Email : fliang@lifetech.com URL:
http://full.negth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI078CG10QPl.
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Meloidogyne hapla
Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
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                                                                                                                                                                                                                                                                                                                                   EST 05-MAY-2003
                                                                                                                                                                                                                                                                                                                                o mRNA linear EST 05-MAY-2003
COT 25-NORMALIZED Homo sapiens cDNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                       DB 10; Length 562;
                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                     BX361013 Homo sapiens PLACENTA COT 25-NORM clone CSODI078YN19 5-PRIME, mRNA sequence. BX361013
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                                                       6.0
           1.3%; Scc. No. 0. 100.0%; Pred. No. 0. Mismatches
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                                                                                                                                                                                                                                                                                                                                   602 bp
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/db_xref="taxon:9606"
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                                                                               Conservative
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                                                       Similarity
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                             Query Match
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Matches 50;
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BX361013
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CF979621
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Homo sapiens (human)
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CK025580
CK025580.1 GI:38551504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/Linn. at: http://image.llnl.gov Series: IRAL Plate: 46 Row: i Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13385599
This clone has the following problem: retained intron.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 637)
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                              Submitted (31-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs.remail.nlh.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                       URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Testicle, mouse"
/clone lib="NIH MGC 169"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6772969"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="Vector: pDNR-LIB"
                                                                                        Mus musculus (house mouse)
Mus musculus
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Danio rerio
                                               BC049569.1 GI:29612485
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Contact: MGC help desk
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/clone_libe_NIH_GGC_10"
/clone_libe_NIH_GGC_10"
/clone_libe_NIH_GGC_10"

Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NIH ZGC 7). Library was constructed by Open Biosystems (HunEsville, AL)."
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BUS98654.1 GI:23250413
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                                                                         Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10AO7 Bethesda, MD 20892
Email: Gapbs.remmail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14822 row: d column: 06
High quality sequence stop: 103.
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1 (Dases 1 to 844)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Infatitutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.k column: 02
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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rative 0; Mismatches 0; Indels
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BE913663.1 GI:10411508
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                                                                                                                                                                                                                                           /tissue type="mixed (pool of 40 RNAs)"
/lab host="NH108 (T1-phage-resistant)"
/lab host="NH108 (T1-phage-resistant)"
/loce=lvector: pNNR-L142 |
/note="vector is properties of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of the care of
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B 1 (bases to 849)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: David N. Louis, N.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Right quality Sequence stop: 568.
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/tissue type="qiioblastoma with BGFR amplification"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                     organism="Homo sapiens"
ity sequence stop: 403.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E 1 (Bases 1 to 865)

E 1 (Bases 1 to 865)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

Localization/Qualifiers

Localization/Qualifiers

Localization/Qualifiers
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/dev_stage="10 months, virgin"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Organ: mammary; vector: pCMV-SPORT6; Site 1: Sal1;
Site_2: NOTI; Cloned unidirectionally. Primer: Oligo dT.
Library. constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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tive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUG51237 892 bp mRNA linear EST 12-JUL-2000 AUG51237 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 892)
Saeaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K., Hata,H., Yamaquchi,R., Tateyama,S. and Sugano,S. Construction of mouse full length-enriched cDNA libraries by
                                                                                                                                                                                            /organism="Homo sapiens"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enritched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.

1. (bases 1 to 883)

1. ("B." B.", Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligo-capping
Unpublished (1999)
Unpublished (1999)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashimhingo.jp/yoken/genbank/
Seq primer: 5' end primer: CTTCTGCTCTAAAAGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 50; DB 13; Length 883; llarity 100.0%; Pred. No. 0.58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (house mouse)
   BX346858
BX346858.1 GI:30379137
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                                                         Homo sapiens (human)
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                                                                            Homo sapiens
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les 50; Conserv
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Matches
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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ACCESSION
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LOCUS
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/lab_host=-round.
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was primed with an oligo(dT) primer
ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a brail adaptor [GTTGGCCTACTGG], digested and
cloned into distinct brails sites of the pWE185-FL3. Xho!
sites just outside the Drail; sites can be used to isolate
the cDNA insert. Size selection was performed to exclude
fragments <1.5 kb. Library was constructed by Sugano et
al.(University of Tokyo, Institute of Medical Science).
CCustom primer used for sequencing: 5' end primer
[CTTCTGCTCTAAAAGCTGG], 3' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
Genoscope - Centra - France
BP 191 91006 ENRY cedex - France
BP 191 91006 ENRY cedex - France
Email: Begref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7394.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAT024ZC12 T02299 l&cluster=7394.f.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOAT024ZC12_T02299_1.
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BX325997 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI082YI06 5-PRIME, mRNA sequence.
BX325997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
1 (Lases 1 to 916)
1 (Annualia; Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%; Score 50; DB 9; Length 892;
100.0%; Pred. No. 0.57;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-ATTCTAGAGGCGGAGGCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech creator SNART kit and size-selected to contain the 0.2-0. Kb size fraction (other fractions present in NIH MGC 142) Library created in the laboratory of M. Brownstein (NIHH, NIH). Note: this is a NIH MGC Library."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria,
1 (bases 1 to 942)
1 (bases 1 to 942)
1 (cruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LinL at:
http://image.lln.gov
Plate: LLCM3062 row: & column: 04
High quality sequence stop: 352.
High quality sequence stop: 352.
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BP 191 91006 EYRY cedex - France
Email: sequedgenoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7394.f For more information about this cluster, see http://www.genoscope.cns.fr
cgi-bin/cluster.cgi?seq=CSOBAA018ZE02_CS01646_l&cluster=7394.f.
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1.3%; Score 50; DB 13;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 50; Conservative 0; Mismatches
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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JOURNAL
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BX326372
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AUTHORS
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       JOURNAL
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KEYWORDS
SOURCE
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                                        COMMENT
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4928.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi/seq-CSOBAF027ZH10 AF02577_1&cluster=4928.r.
Contact : Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAF027ZH10_AF02577_1.
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//db xref="taxon:5606"
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                                                                                                                                                                                                                                                                                                              EST 08-MAY-2003
                                                                                                                                                                                                                                                                                                       BX369283

BX369283 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI054YM17 5-PRIME, mRNA sequence.
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1. (bases 1 to 940)
1. (Jases, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 942)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 10546264 NIH MGC_141 Homo sapiens cDNA clone
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1.3%; Score 50; DB 13; Length 940;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 50; Conservative 0; Mismatches 0; Indels
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Genoscope - Centra National de Sequencage
Genoscope - Centra National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4928.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CSOBAPC27ZH10 AF02577_2&cluster=4928.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faradax Avenue Genoscope sequence ID : CSOBAFC27ZH10_AF02577_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X369284 952 bp mRNA linear EST 08-MAY-2003 X369284 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA LONE CSODI054YM17 5-PRIME, mRNA sequence.
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//organism="Homo sapiens"
//db itype="mkna"
//db xref="taxna"
//db xref="taxna"
//dlone="CSODIO82YIO6"
//dlone="CSODIO82YIO6"
//dlone lib="PlackBryA COT 25-NORWALIZED"
//olone lib="Homo sapiens PlackBryA CO
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/mol_type="mRNA"
/fususe_type="mRNA"
/tissuse_type="mRACENTA COT 25-NORMALIZED"
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/note="lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib="top prime end enriched with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and SCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                               http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAA0182E02_CS01646_1.
Location/Qualifiers
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100.0%; Pred. No. 0.53;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.54;
iive 0; Mismatches 0; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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994 bp mRNA linear EST 05-FEB-2002
AGENCOURT 6417960 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534247
57, mENA sequence.
BX369858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI006YN18 5-PRIME, mRNA sequence.
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1 (bases 1 to 956)
1 (Liw.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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1 (bases 1 to 994)
NHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR vites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
BE 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3779.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg-cc08AG0252A03_CS02321_1&cluster=3779.r.
cgi-bin/cluster.cgi?seg-cc08AG0252A03_CS02321_1&cluster=3779.r.
Contact: Feng Liang Email: fliangellfetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0BAG025ZA03_CS02321_1.
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Email: cgapbs-r@mail.nih.gov
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Note: this is a NIH_MGC Library."
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

B. (1988) 1.0.1023)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at:

http://image.llml.gov
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/werage insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
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602368921F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4477133 5',
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1220 row: g column: 16
High quality sequence start: 28
High quality sequence stop: 412.
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100.0%; Pred. No. 0.51;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
    Tissue Procurement: ATCC
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BG254352.1 GI:12764168
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602312366F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4422088 5',
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium (LINL)
http://image.llnl.gov
Plate: Library Column: 17
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AGENCOURT_10173174 NIH_MGC_144 Mus musculus CDNA clone IMAGE:6534925 5', mRNA sequence.
Query Match
1.3%; Score 50; DB 12; Length 1023;
Best Local Similarity 100.0%; Pred. No. 0.5;
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100.0%; Pred. No. 0.49;
ive 0; Mismatches 0; Indels
                                                                                   High quality sequence stop: 444.
Location/Qualifiers
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Search completed: April 23, 2004, 11:01:47 Job time : 8962 secs

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AK12551 Homo sapi
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AC104556 Plasmodiu
AC104510 Mus muscu
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AC124656 Mus muscu
AC134656 Homo sapi
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AC165163 Homo sapi
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AC18266 Rattus no
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AC110189 Mus muscu
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AC13131081 Mus muscu
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1 MGNYLLRKLSCLGENQKKPK......svsrpcscthehdyevvFPH
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                               - nucleic search, using frame_plus_p2n model
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BC024174

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Nocka,K., Pirozzi,G. and Einstein,R.
Novel genes associated with allergic hypersensitivity and mast cell
activation WO 0246389-A 1 13-JUN-2002;
UCB, S.A. (BE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GlySerGlySerGluGluValCysTyrThrVallleAsnHislleProHisGlnArgSer
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/note="unnamed protein product"
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1. 3762
Apparism="Homo sapiens"
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Sequence 1 from Patent WO0246389.
AX505122
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

1. (bases 1 to 2648)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Zeeberg, B., Buetow, K.H., Schamen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schamen, C.M., Schuler, G.D.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Maruslana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Norley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellon, B., Ketteman, M., Madan, A., Scher, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myes, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
M. Mann, J. Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 32 Row: b Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21687148.
Location/Qualifiers
                                                  BC024174 2648 bp mRNA linear PRI 04-OCT-2003
Homo sapiens LOC148823, mRNA (cDNA clone MGC:24564 IMAGE:4109064),
complete cds.
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Direct Submission
Submitted (19-PEB-2002) National Institutes of Health, Mammalian
Submitted (19-PEB-3002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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NHF-WGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATC

CONA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

http://www.systemsbiology.org

contact: amadan@systemsbiology.org

Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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48. .455
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BC024174.1 GI:18848218
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RERSETEYALLRISVSRPCSCTHEHDYEVVFPH"
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Shichata,N., Matsumcto,K., Hirano,M., Sano,S., Nomura,R.,
Shichata,N., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
Yoshikawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,
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Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
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Oshima,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T., Sugano,S.,
Unpublished
E 2 (bases 1 to 1709)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GlySerGlySerGluGluValCysTyrThrValileAsnHisileProHisGlnArgSer 80
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens cDNA FLJ41804 fis, clone NOVAR2000710.
AK123798
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Oligo capping; fis (full insert sequence).
Momo sapiens (human)
Homo sapiens
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Matches:
Conservative:
Mismatches:
Indels:
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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JOURNAL
REFERENCE
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Isogai,T. and Yamamoto,J.

Direct Submission

Bundtted (15-7UL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mall:genomics@hri.co.jp, Tel:181-448-52-3975, Fax:181-438-52-3986)

REDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Balocechnology (RAB); CDNA fibrary

construction: Halix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB;

HRI, and Blotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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Macaca fascicularis brain cDNA clone:QtrA-14007, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="vvary"
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/dev stage="adult"
/note="cloning vector: pME18SFL3"
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AB060908
AB060908.1 GI:13874585
Oligo capping, fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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/db_xref="taxon:9606"
/clone="NOVAR2000710"
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Kareuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Oteuki,T., Sato,H., Wakamatsu,A., Ishi,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa, K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,K., Kanehori,K., Takahashi-Fujii,A.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                               350 GIGIGCTACACTGTCATTAATCACATCCCCCATCGGAGGTCTTCCCTGAGGCTCCAATGAT 409
                                                                                                                                                                                                                                                                                                                                                                                                                               107 GluThrGluTyrAlaLeuLeuArgThrSerValSerArgProCysSerCysThrHisGlu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 AGCAAAGAAGTTTCATCCATTTCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAA 349
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                       410 GATGGCTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGAGAATTTAGAGAAAGGTCA
                                                                                                                                                                                                                                                                                                       87 AspGlyTyrGluAsnIleAspSerLeuThrArgLysValArgGlnPheArgGluArgSer
                                          SerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySerGluGlu
                                                                                                                                                                     67 ValCysTyrThrValileAsnHisIleProHisGlnArgSerSerLeuSerAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AO32 bp mRNA linear
Homo sapiens cDNA FLJ44728 fis, clone BRACE3024537.
AK126682
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/mol type="mRNA"
/db xref="texon:9606"
/clone="BRACE3024537"
/clone Tib="BRACE3"
/clone Tib="BRACE3"
/note="cloning vector: pME18SFL3"
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Oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 HisaspTyrGluValValPheProHis 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 CATGATTACGAAGTTGTGCTTCCACAC 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.02e-51
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AK126682
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                                                                                                                              Geada, N., Hida, M., Kusuda, J., Tanuma, R., Hirata, M., Hirai, M.,

Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.

Prediction of unidentified human genes on the basis of sequence similarity to novel cDNAs from cynomolgus monkey brain online Publication

Conline Publication

Online Publication

(Canome Biology 2001 3(1): research0006.1-0006.5,

http://genomebiology.com/2001/3/1/research/0006/

2 (bases 1 to 1924)

Rashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.

Direct Submission

Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

(B-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, 15-181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poetor: pMEBS-FL3 (Acc.No. AB009864)
R. Sitel: Drall (CACTGTGTG)
R. Sitel: Drall (CACTGTGTG)
Description: 1st strand CACATGTGTG)
Lossription: 1st strand CACATGTG)
Lossription: 1st strand CACATGTG)
Lossription: 1st strand cDNA was primed with an oligo(dT) primer farging specific's and 3 primers and amplified by PCR. The PCR outling specific's and 3 primers and amplified by PCR. The PCR acclude fragments <1.5kD.The Sfil and size selection was performed to exclude fragments <1.5kD.The Sfil-digested PCR product was cloned into distinct Drall sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., Institute of Medical Science, University of (Sugano et al., Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTFERKIQDODKKSKBVSSISNQENENGSGSEEVCYTVINHIP HRRSSLSSNDDGYENIDSLTRKVREFRERSFTEYALLRTSVSRPYSCTHEHDYEVVLP H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 GAAAGAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLysLysGlyAsnProAspGlu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GluarglysArgGlnGluMetThrThrPheGluargLysLeuGlnAspGlnAspLysLys 46
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue type="temporal lobe right" clone_lib="macaque brain cDNA library QtrA" dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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Conservative:
Mismatches:
Indels:
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"mol type="mRNA"
db xref="taxon:9541"
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/protein_id="BAB46903.1"
/db_xref="G1:13874586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Custom primer used for sequencing (5' end primer (CTTGGTCTAAAAGCTGCG) 3' end primer [CGACTGCAGCTCGAGCACA] ) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
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The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 141268) Waterston, R.H.
organism="Homo sapiens"
                                                                                                                                                        note="unnamed protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-4136)
                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                          clone="BRACE3002390"
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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581.00
85.19%
84.44%
81.26%
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Best Local Similarity:
Query Match:
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S Dieses I to 4136)

S Isogai, T. and Yamamoto, J.

Direct Submission

Direct Submission

Submitteed (15-JUD-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-malligenomicséhrinor), Telis-1438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA ilbrary

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center for); 5- & 3-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 09-SEP-2003
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Kodaira, H., Furnya, T., Takahashi, M., Kikwa, B., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Osto, K., Yamazaki, M.,
Sugiyama, T., Irafe, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Nobima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
NEDO human oDNa sequencing project
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                    1 MetGlyAsnTyrLeuLeuArglysLeuSerCysLeuGlyGluAsnGlnLysLysProLys 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GlySerGlySerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer
                                                                                                                                                                                                                               41 GlnAspGlnAspLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsn
                                                                                                                                                                                                                                                                                                                          437 CAAGAICAAGAIAAGAAAAGCCAAGAAGIIICAICCACIICIAAICAGGAAAACGAGAAI
                                                                                                                                                                                                      21 LysGlyAsnProAspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeu
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HOMO Bapiens CDNA FLJ42529 fis, clone BRACE3002390.
AK124520
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Oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
Mismatches:
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                                                                               US-10-005-907-2 (1-135) x AX126682 (1-4032)
  85.19%
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COMMENT

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141268 bp DNA linear HTG 23-SEP-2000 HOMO sapiens chromosome 1 clone RP11-115C4, WORKING DRAFT SEQUENCE, AC074365
                                                                                                              /codon_start=1
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NPPRWSETQELRNRVTVKRWEIISCENSGRK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro 120
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141268)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAspGlnAspLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 caagarcaagaraagaaaagccaagaagrrrcarccacrrcraarcaggaaaacgagaar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlySerGlySerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LysGlyAsnProAspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysserCysThrHisGluHisAspTyrGluValValPheProHis 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  798 IGITICCTGCACCCATGAGCATGATATATGAAGTTGTGTTTCCACAC 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        498 Ardccaaaarrarcrccrccaaaaacrc-------
/tissue type="cerebellum"
/clone lib=BRACE3"
/noce="cloning vector: pME18SFL3"
136. 537
                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Direct Submission

Cambridgeshire, CB10 18A, UK. B-mail enquiries:

Cambridgeshire, CB10 18A, UK. B-mail enquiries:

Cambridgeshire, CB10 18A, UK. B-mail enquiries:

humquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 24, 2002 this sequence version replaced gi:18121511.

During sequence assembly data is compared is used overlapping clones.

Where differences are found these are annotated as variations

rogether with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

10); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em: EMBL; Sw:,

SWISSPROT; TI:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL606804 11near PRI 23-OCT-2002
Human DNA sequence from clone RPI1-978I15 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 SerValSerArgProCysSerCysThrHisGluHisAspTyrGluValValPheProHis 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 185467)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5700 CAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGAGTGTGCTACACTGTCATTAATCACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 ThranglysValArgGlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5580 ACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GlnGluAsnGluAsnGlySerGlySerGluGluValCysTyrThrValIleAsnHisIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 ProHisGlnArgSerSerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeu
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Matches:
Conservative:
Mismatches:
/note="assembly_name:Contig6"
100501. .111915-
%note="assembly_name:Contig7"
112016. .125713
/note="assembly_name:Contig8"
125814. .141268
/note="assembly_name:Contig9
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vector_side:left"
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Homo sapiens
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Best Local Similarity:
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DB:
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       Direct Submission
Submitted (29-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Markway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                              Sep 23, 2000 this sequence version replaced gi:9838075.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: minary 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 138274 bases at least Q40
Consensus quality: 138356 bases at least Q30
Consensus quality: 139182 bases at least Q20
Insert size: 142000; agarose-fp
Insert size: 142000; agarose-fp
Quality coverage: 4.64 in Q20 bases; sum-of-contigs
Quality coverage: 4.81 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31377: contig of 31377 bp in length 31477: gap of unknown length 63011: contig of 31534 bp in length 63011: gap of unknown length 64845: contig of 1734 bp in length 64945: gap of unknown length 6706: contig of 2661 bp in length 67704: contig of 9968 bp in length 77674: contig of 9968 bp in length 77774: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 11482 bp in length gap of unknown length contig of 1144 bp in length contig of 11415 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length gap of unknown length
                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
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note="assembly_name:Contig10"
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note="assembly name:Contig11"
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note="assembly_name:Contig2"
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89357. .100400
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/organism="Homo sapiens"
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                                                                                                                                                                                                                    Genome Center
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.rdmail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing by: National Institutes of Health Intramural
Sequencing by: National Institutes of Health Intramural
Sequencing by: National Institutes of Health Intramural
Sequencing Contact: Nacyland;
Neb site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Contact: nisc.mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Hadpighi,P.,
Maduro,O.L., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Maskerl,B., Mask
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22749536.
Location/Qualifiers
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ABEYYENVPCKABRPRESLGGTETEXSLLHMPSTDPRHARSPEDEYELLMPHRISSHP
LQOPRPLMAPSETQFSHL"
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Bouffard, G.G., Brakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Sakalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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protein id="AAH30506.1"
db_xref="G1:2099180"
db_xref="LocusID:257144"
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/db_xref="LocusID:257144"
/db_xref="MIM:607792"
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'clone_lib="NIH_MGC_85"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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qene="GCET2"
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Strausberg, R.
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                                                  was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP11-978115 is from the library RPC1-11.4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Homo sapiens germinal center expressed transcript 2, mRNA (cDNA clone MGC:40441 IMAGE:4385178), complete cds.
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                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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/db_xref="texor:9606"
/chromosome="1"
/clone="RP11-978115"
/clone="RP11-978115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Homo sapiens
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Best Local Similarity:
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1 (bases 1 to 1654)
Lossos,I.S., Alizadeh,A.A., Rajapaksa,R., Tibshirani,R. and Levy,R. HGAL is a novel interleukin.4-inducible gene that strongly predicts Blood 101 (2), 433-440 (2003)
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                                                                                                                                                                                                                                                                                                                                114 GAAGGGTGTTTCTGCCTTCCATGGAAAAAATACTCATTTTTGAAAAAAAGGG---CAAGAT 230
                                                                                                                                                                                                                                                                                                  231 TCCCAAAACGAAAATGAAAGAATGTCATCTACTCCCATCCAGGACAATGTTGACCAGGACC 290
                                                                                                                                                                                                                                                                                                                                                                                                    54 ATGGGAAATTCTCTGCTGAGAAAAAAAGGGGGGGAGGAGAAGACACTCAAGAGATGCCTTGG 113
                                                                                                                                                                                                                                                                                                                                                                                    LeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArgGln 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUN-2002) Division of Oncology, Department of Medicine, Stanford University, 269 Campus Drive, CCSR building, Room 1100, Palo Alto, CA 94305-5151, USA Location/Qualifiers
                                                                                                                               MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysPro---
                                                                                                                                                                                                                                -------GlnGluMetThrThrPheGluArgLysLeuGlnAsp
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                                                                                                                                                                              -----LysLysGlyAsnProAspGluGluArgLysArg-----
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Conservative:
Mismatches:
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Jossos, I.S., Alizadeh, A.A. and Levy, R. Nirect Submission
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              2.76e-08
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LQQPRPLMAPSETQFSHL"
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1 (bases 1 to 3270)

1 (bases 1 to 3270)

1 (bases 1 to 3270)

2 (ban, Z., Shen, Y., Du, C., Zhou, G., Rosenwald, A., Staudt, L.M., Greiner, T.C., McKeithan, T.W. and Chan, W.C.

Two newly characterized germinal center B-cell-associated genes, necella and GCET1 and GCET2, have differential expression in normal and necellastic B cells

Am. J. Pathol. 163 (1), 135-144 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AATGTGAGAATGCAAAGCCCCAAACAGAGAACATCCAGATGCTGGGATCACCATATCGCT
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nodified ITAM motif, similar to mouse M17"
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                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hillman,J.L., Jones,A.L., Yu,J.Y., Wright,R.J., Gietzen,D., Li
Yap,P., Dahl,C.R., Momiyama,M.G., Bradley,D., Rohatgi,S.,
Harris,B., Roseberry, Ann,M., Gerstin,B.H., Peralta,C.H.,
David,M.H., Panzer, Scott,R., Flores,V., Daffo,A., Marwaha,R.,
Scretcy, molecules
Patent: WO 02020756-A 4614-MAR-2002;
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Matches:
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                                                           AX740457 1643 bp
Sequence 46 from Patent WO02020756.
AX740457
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   Location/Qualifiers
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LQQPRPLMAPSETQFSHL"
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MI7; similar to MGC40441 sequence in GenBank Accession.
Number BC030506"
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                                                                                University of Nebraska Medical
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Stan, Z., Shen, Y., Du, C., Zhou, G., McKeithan, T., Rosenwald, A., Staudt, L. and Ghan, W.C.
Direct Submission
Submitted (07-JAN-2003) Pathology, University of Nebraska McCenter, #42, Omaha, NB 69198, USA
Location/Qualifiers
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// Cell line="DHL16"

// Cell sapiens"
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Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa Kamatari, Kisarazu, Chiba 292-0818, Japan

(R-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5-6 and one pass sequencing: RAB;

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irle, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Salto, K., Nishikawa, T., Kimura, K., Yamashita, H., Magatsuma, M., Mekamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNa sequencing project
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                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                    Homo sapiens CDNA FLJ43533 fis, clone PLACE7001544. AK125521. AK125521.1 GI:34531645 Glub Capping; fis (full insert sequence). Homo sapiens (human) Homo sapiens (human).
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19
31
2
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/clone Tib="PLACE7"
/note="cloning vector: pME18SFL3"
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Matches:
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="PLACE7001544"
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gai, T. and Yamamoto, J.
                              475 TATGAACTTCTTATGCCC 492
129 TyrGluValValPhePro 134
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AK125521/c
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/db_xref="GI:1262852"
/tb_xref="GI:1262852"
/tb_xref="GI:1262852"
/tb_xref="GI:1262852"
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/tb_stanlaufon="MONCOMORY FOR MONCOMORY FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOWORD FOR MONTOW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATICGGITCTCCGTTTTCCCTTCTCCCTCAGGCCCTACCTTCCACA---GATGATGAA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAsnileAspSerLeuThrArgLysValArgGlnPheArgGluArgSerGluThrGlu 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 GAGAACATCTCTAACAAGGCTGAGAGACACAAAGAGTCTTCAAGAGGAACAGAGACTGAG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyralaLeuLeuArg---ThrSerValSerArgProCysSerCysThrHisGluHisAsp 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-AUG-1994) Robert C. Rickert, Institute for Genetics,
University of Cologne, Weyertal 121, Cologne, 50823, Germany
Location/Qualifiers
1. 1672
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Rodentia; Rodentia; Rodentia; Muridae; Murinae; Mus. 1 (bases 1 to 1672)
Christoph, T., Rickert, R. and Rajewsky, K.
M17: a novel gene expressed in germinal centers
Int. Immunol. 6 (8), 1203-1211 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluVal 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 SerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySerGluGluValCySTyrThr
                                                       linear
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                                                          mRNA
                                                       MMU13263
Mus musculus M17 mRNA, complete cds.
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/product="M17 protein"
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                                                                                                                                                                                              Mus musculus (house mouse)
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94. .573
/gene="M17"
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/gene="M17"
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Rickert, R.C.
                                                                                                                 U13263
U13263.1 GI:533130
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RESULT 13
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Submitted (26-AUG-2002) Human Genome Sequencing Center, Department of Moleular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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31707. .31920
/etandard_name="G44369"
32757. .33036
/etandard_name="D11S3206"
88551. .68832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard_name="SHGC-112515"
1827. .71979
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/standard_name="SHGC-68798"
77907. .7<u>8</u>053
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
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                                                     Baylor Plaza, Houston,
4 (bases 1 to 81001)
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alaboroks, S.L., Amaratunge, H.C., Aked, R.W., Ayele, W., Banks, T., Barbaria, J. Briecon, J. Binage, K., Blankenburg, K., Bonnin, D., Bouck, J. Bowies, S., Brieva, M., Brown, E., Brown, M., Barks, T., Barbaria, J. Bouck, J. Bowies, S., Bracton, J. Brieston, D. Baryat, N.P., Bhuch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chavez, D., Carcon, T.F., Carter, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Cayle, M.D., Torderich, D., He, X., Daladov, D., Edward, C., Elhaj, C., Escotto, M., Douthwaite, K.J., Davis, C., Carrell, M., Guevara, W., Gunzatne, P., Hale, S., Hamilton, K., Harnide, K.J., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Hawes, A., Harnandez, J., Hernandez, J., Hanses, M., Holloway, C., Kratovic, J., Karliy, S., Khan, U., Klug, L., Kovar, C., Kratovic, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Moorish, T., Morris, M., Morse, M., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Moorish, T., Sodergen, B., Prikmes, P., Prikmes, P., Prikmes, P., Prikmes, S., Primms, S., Primms, S., Primms, S., Primms, S., Primms, S., Primms, S., Primms, S., Staton, J., Soders, S., Soder, S., Soder, R., Walley, S., Walley, S., Walley, S., Wall
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115 ThrSerValSerArgProCysSerCys---ThrHisGluHisAspTyrGluValValPhe 133
                                                                                                                                                                                                                                                            Homo sapiens 3 BAC RP11-757F18 (BAC Library) complete sequence.
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Direct Submission
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches
GTSS are identified using ePCR (Genome Res. 7:541-550) searches
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consenus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
Worley, K.C.
Direct Submission
Submitted (30-AUG-2002) Human Genome Sequencing Center, Department
Submitted (30-AUG-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 30, 2002 this sequence version replaced gi:22475264.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1. .2041)
/note="overlaps bases 1. .2041 of clone AC119734"
/function="clone overlap"
11149. .11300
/standard_name="RH65506"
/note="Size confirmed by PCR and regriction digest."
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/standard_name="RH93661"
77944. .78073
/standard_name="SHGC-59894"
78015. .91001
/note="overlaps bases 1. .2988 of clone AC024887"
/function="clone overlap"
                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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126.00
59.76%
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Best Local Similarity:
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US-10-005-907-2 (1-135) x AC128688 (1-81001)

75 IlebroHisGlnArgSerSerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSer 94 ò 셤 ઠે ઠે g

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Search completed: April 22, 2004, 17:57:43 Job time: 2245 secs

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April 22, 2004, 11:26:15; Search time 1784 Seconds (without alignments) 9839.646 Million cell updates/sec
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1 atgggaaattatctcctgcg......atgaagttgtgtttccacac 405
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ACCESSION VERSION		BC024174 BC024174	2. ⊷.	. H	:18848		
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	ORGANISM			sapiens yota; M lia; Eu	ens ; Metazoa; Eutheria;	, p	Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;	rata; Buteleostomi; nidae; Homo.
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_			Klausne	н Ж	.α.	111	; w	Σ

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PAT 27-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 CAGITITAGAGAAAGGTCAGAGACAGAATAIGCCCTICTIAGGACTICIGTIAGTAGGCCT 360
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                                            48 ATGGGAAATTATCTCCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAAGCCCCAAG 107
                                                                                                                                                  121 CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT 180
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Patent: WO 0246389-A 1 13-JUN-2002;
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1. 3762
/organism="Homo sapiens"
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Sequence 1 from Patent W00246389
AX505122
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., More, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loucullano, N.P., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Male, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Murany, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Onnes, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 32 Row: b Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21687148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xrefe"Locusid:148823"
/translation="MGNY1LEXLSCIGENOKKPKKGNPDEERKROEMTTFERKLODOD
KKGQEVSSTSNQENENGSGESPCYTVINHIPHQRSSLSSNDDGYENIDSLTRKVRQF
RERGETEYALLRTSVRAPCSCTHEHDYEVVPH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (19-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Betheada, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Produrement: ATC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahay, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:24564 IMAGE:4109064"
/tissue_type="Bone marrow, acute myelogenous leukemia"
/clone_lib="NXH MGC_55"
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/codon_start=1
/product="LOC148823"
/protein_id=RAAH24174.1"
/db_xref="GI:18848219"
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/gene="LoC148823"
/db_xref="LocusID:148823"
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/organism="Homo sapiens"
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Coada,N., Hida,M., Kusuda,J., Tanuma,R., Hirata,M., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.

Prediction of unidentified human genes on the basis of sequence
similarity to novel cDNAs from cynomolgus monkey brain
Online Publication
( Genome Biology 2001 3(1): research0006 1-0006, 5;
http://genomebiology.com/2001/3/1/research/0006/
E. Chases 1 to 1924)
Direct Submission
Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
(E-mail:khashiganih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB060908 1924 bp mRNA linear PRI 10-JAN-2002 Macaca fascicularis brain cDNA clone:QtrA-14007, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 CAGTITTAGAGAAAGGICAGAGACAGAATATGCCCTTCTTAGGACTTCTGTTAGGCCT 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                       239 GGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCTGAGCTCCAATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGA
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                                                                                                                                                             59 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAG
                                                                                                                                                                                                                                                                     121 CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT
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                                                                                                          1 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAAGAAGAAGCCCAAG
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        Length 1709;
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Score 403.4; DB 9;
Pred. No. 2.6e-93;
0; Mismatches 1;
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Draili (CACTGTGTG)
Draili (CACCATGTG)
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AB060908.1 GI:13874585
Oligo capping; fis (full insert sequence)
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
     99.6%;
                              Best Local Similarity 99.8 Matches 404; Conservative
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R. Site2:
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S Gogai, T. and Yamamoto, J.

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mailigenomics@hri.oc.jp, Telisla, 1438-52-395; Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA ilbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5-c 3-end one pass sequencing: RRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

RAB; annotation: HRI and RAB.
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        CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT 180
                                                                                                                                                             205 GGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCC 264
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                                                                                                                                                                                                                                                                                                                                                               325 CAGITIAGAGAAAAGGICAGAGAAAAAATAIGCCCTICTIAGAACTICTGIIAGIAGGCCT 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                       145 CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT
                                                                                                          GGCAGTGGTTCTGAAGAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCC
                                                                                                                                                                                                                  TCCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGA
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Homo sapiens cDNA FLJ41804 fis, clone NOVAR2000710.
AK123798
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/tissue type="cvary"
/clone lib="NOVAR2"
/dev stage="adult"
/note="cloning vector: pME185FL3"
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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/db_xref="taxon:9606"
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Xamihara, K., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katenta, N., Saro, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakametsu, A., Ishii, S., Kamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Marsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Wurakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Kawakami, B., Suzuki, Y., Sugano, S., NEDO human cDNA sequencing project Isogai, T.
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HOMO sapiens cDNA FLJ42529 fis, clone BRACE3002390.
AK124520.1 GI:34530224
AK124520.1 GI:34530224
Olio capping; fis (full insert sequence).
Homo sapiens (human)
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/mol type="mRNA"
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/tissue_type="cerbellum"
/clone lib="BRACB3"
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                                                   the Drall sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method forgano et al., , Institute of Medical Science, University of Tokyo).

Custom primer used for sequencing (5' end primer [CCAACTGCGTCAAAAGCTGCG];
3' end primer [CCAACTGCAGCACAA]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue type="temporal lobe right" /clone_lib="macaque brain cDNA library QtrA" /dev giage="adult" |
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Pred. No. 5.5e-82;
0; Mismatches 21;
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Best Local Similarity 94.7%;
Matches 372; Conservative 0
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ACU/4365 141268 bp DNA linear HTG 23-SEP-2000 Homo sapiens chromosome 1 clone RP11-115C4, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Bases 1 to 141268)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MMC 63108, USA
On Sep 23, 2000 this sequence version replaced gi:9838075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center code: WUGSC
  795 CCTIGITCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCCACAC 842
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unknown length
of 13698 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                              The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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contig
gap of
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Waterston, R.H.
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be preserved
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SOURCE
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Sister to 4136)

Sister to Administration of the following project (HRI Team); 2-6-7

Bloogal, T. and Yamamoto, J.

Direct Submission

Submitted (15-JUJ-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mall igenomics@hri.or.jp, Telis1-438-52-3976, Pax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

[Location/Qualifiers]
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NFPRWSETQELRNRVTVKRWEIISCENSGRK"
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                                                           Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kadalra, H., Furuya, T., Takahashi, M., Kikkawa, B., Cmura, Y., Abe, K.,
Kadihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A.,
Kamamoto, J., Isono, Y., Kawai-Hio, Y., Sato, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fuji, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
NEDO human cDNA sequencing project
Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue type="cerebellum"
clone lib="BRACE3"
note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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/clone="BRACE3002390"
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cumboringsanier. ac.uk clone requests clonerequestGasanger.ac.uk on oct 24, 2002 this sequence version replaced gi:1812151.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation and y not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the feature table with their source databases: Em; EMBL; Sw; Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping chromosome 1 Mapping abreauting and the found at the feature table with the shanger Centre Chromosome 1 Mapping chromosome 1 Mapping abreauting and a preview of the manner of an he found at the found at the found at the feature table with the sanger Centre Chromosome 1 Mapping abreauting and the found and the found and the found and the found at the feature table with the found at the feature table with the found at the feature farmed from part of bacterial clone contigs of human part of bacterial clone contigs of human part information and the found at the feature farmed and the feature table with the found at the feature farmed and the feature farmed and the farmed and the farmed and the farmed and the farmed and the farmed and the fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP11-978115 is from the library RPCI-11.4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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1. .185467
/organism="Homo gapiens"
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clone="RP11-978115"
clone_lib="RPCI-11.4"
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Human DNA sequence from clone RP11-978I15 on chromosome 1, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (16-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITCATCCACTTCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACA
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0
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Pred. No. 9.4e-52;
0; Mismatches 10; Indels 0;
4 141268: contig of 15455 bp in length.
Location/Qualifiers
1. .141268
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77775. .10400
89357. .10400
7001. .101915
100501. .111915
7001. .101915
                                                                                                                                                                                                                                                                          note="assembly_name:Contig11"
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note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                            63112. .64845
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                                                                                                                                                                                                                                                                                                                                           64946. 67606 -- /note="assembly_name:Contig3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig8"
25814. .141268
note="assembly_name:Contig9
                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_name:Contig4"
                                                         1.141268
| Organism="Homo sapiens"
| mol_type="genomic DNN" |
| db_xref="texcon:9606" |
| chromosome="1" |
| clone="RP11-115C4"
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1 (bases 1 to 185467)
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Homo sapiens
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Best Local Similarity 96.11
Matches 247; Conservative
       125814
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TITLE
JOURNAL
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AL606804
LOCUS
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION ACCESSION

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DENKATYOLE, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 165).

Lossoo, I.S., Alizadeh, A.A., Rajapaksa, R., Tibshirani, R. and Levy, R. HGAL is a novel interleukin-4-inducible gene that strongly predicts Burvival in diffuse large B-cell lymphoma
                                                                                                                                                                                                                                                                                                                  /Godon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 CGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 TCAGAGATCCTCCCTGAGCTCCAATGATGGCTATGAGAACATTGACTCCCTCACAAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 GAAAGTGAGACAGTTTAGAGAAAAGGTCAGAGAGAGAAATATGCCCTTCT---TAGGACTTC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 rerreaccasaccracrcadasascrereiraraccricarcaarcarcaserressiters 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 dagacccadadadrecrrgdgadadadredadrendararreacriteracarardecerre 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 TACAAGGCCATCAGGGAACTCTGCTGAAGAGTACTATGAGAATGTTCCCTGCAAAGCTGA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 TGTIAGTAGGCCTTGTTCCTGCACCCATGAGGATGATTATGAAGTTGTGTTTCCACAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lossos, 1.S., Alizadeh, A.A. and Levy, R.
Liossos, 1.S., Alizadeh, A.A. and Levy, R.
Direct Submission
Submitted (16-JUN-2002) Division of Oncology, Department of
Medicine, Stanford University, 269 Campus Drive, CCSR building,
Room 1100, Pallo Alto, CA 94305-5151, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 58; DB 9; Length 1532;
llarity 54.4%; Pred. No. 0.00023;
Conservative 0; Mismatches 130; Indels
                                                                                                                                       /note="synonyms: HGAL, GCAI2, MGC40441"
/db_xref="LocusID:257144"
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Homo sapiens HGAL mRNA, complete cds.
AF521911.1 GI:27733682
                                       'note="Vector: pCMV-SPORT6
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/db_xref="taxon:9606"
'lab host="DH10B"
                                                                                                                      gene="GCET2"
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Matches 162;
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Tissue Procurement: Lou Staudt
Tissue Procurement: Lou Staudt
Tissue Procurement: Lou Staudt
Tissue Procurement: Lou Staudt
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaitherseburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcanhgri.nih.gov
Akhter.N. Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., (Juan,X., Gupta,J., Haghighl,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                 In (Dates 1 to 1924).

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Wang, J., Hsieh, R.F.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, R.F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.B., Bonaldo, M.F., Casarant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Munny, D.M., Soder, S.M., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and mouse cDNA sequence
M.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: a Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 22749536.
Location/Qualifiers
                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1532)

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Submitted (07-MAX-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
    Homo sapiens germinal center expressed transcript 2, mRNA (cDNA clone MGC:40441 IMAGE:4385178), complete cds.
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Contact: MGC help desk
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tissue type="Lymph, lymphoma"
/clone_lib="NIH_MGC_85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R.
                                                                                                                                                                                                                                                             Homo sapiens
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

FEATURES

PRI 14-JAN-2003

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mRNA

Gaps

174

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Query Match Local

ORIGIN

Best Loca Matches

231

291

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g ð 요 VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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REFERENCE AUTHORS

JOURNAL MEDLINE

TITLE JOURNAL

FEATURES

LOCUS

AY212246

RESULT

ACCESSION

CDS

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/codon_profile | Conter | Codon_start=1
/product=1 | Codon_start=1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 28-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 IGTIAGIAGGCCTIGITCCTGCACCATGAGCATGATTATGAAGTTGTGTTTCCACAC 405
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12.1%; Score 49; DB 6; Length 7218;
Best Local Similarity 2.2%; Pred. No. 0.039;
Matches 7; Conservative 192; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.3%; Score 59; DB 9; Length 3270; Best Local Similarity 54.4%; Pred. No. 0.00021; Matches 162; Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
1. .7218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQQPRPLMAPSETQFSHL'
. .3270
gene="GCET2"
                                                                     note="GCAT2"
                                                                                                                                    gene="GCET2"
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VERSION
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AY212246
                                                                                                                                                                            /protein_id="AAO21701.1"
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CLPWKXILIFEKRQDSQNENERMSSTPIQDNVDQTYSEELCYTLINHRVLCTRPSGNS
AEEYYENVCKAERPESLGGTETEYSLLHMPSTDPRHARSPEDEYELLMPHISSHF
LQQPRPLMAPSETQFSHL"
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1 (bases 1 to 3270)

2 Shen, Y., Du,C., Zhou,G., Rosenwald, A., Staudt, L.M., Greiner, T.C., McKeithan, T.W. and Chan, W.C.

Two newly characterized germinal center B-cell-associated genes, GCET1 and GCET2, have differential expression in normal and neoplastic B cells

Am. J. Pathol. 163 (1), 135-144 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGAATGGCAGTGCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                    /note="germinal center-associated lymphoma; contains modified ITAM motif, similar to mouse M17"
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Pan.Z., Shan,Y., Du.C., Zhou,G., McKeithan,T., Rosenwald,A., Staudt,L. and Can,W.C.
Direct Submission
Submitted (07-JAN-2003) Pathology, University of Nebraska McCenter, #42, Omaha, NE 68198, USA
Location/Qualifiers
1. .3270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    atch 14.3%; Score 58; DB 9; Length 165 Lal Similarity 54.4%; Pred. No. 0.00023; Lonservative 0; Mismatches 130; Indels
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/cell_line="DHL16"
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AY212246.1 GI:27948576
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gap of 100 bp
contig of 2396 bp in length.
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vector side:left"
3753. _18203
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fragment chain:1"
18304. .31101
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/clone_lib="DanioKey"
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note="assembly_fragment:00186
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4898. .44797
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ragment_chain:2"
6105. .73586
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ragment chain:2"
3687. .76188
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ragment_chain:2"
32193. .97210
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ragment chain:1"
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ragment_chain:2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                   BX855623 177229 bp DNA linear HTG 08-DEC-2003
Danio rerio clone DKEY-283F18, *** SEQUENCING IN PROGRESS ***, 23
                                                                                                                                                                             247 AGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGACAGTTT 306
                                                                                           187 GGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCTCCCTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cyptinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyptinidae; Danio.
1 (bases 1 to 177229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (07-DSC-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. B-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                127 CAAGATAAGAAAAGCCAAAGATTTCATCCACTTCTAATCAGGAAAACGAGAATGGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator; 100% of reads
Consensus quality: 16428 bases at least Q40
Consensus quality: 170485 bases at least Q30
Consensus quality: 172162 bases at least Q30
Insert size: 175629; sum-of-contigs
Insert size: 184442; 3.0% error; agarose-fp
Quality coverage: 4.56x in Q20 bases; sum-of-contigs Quality
coverage: 4.48x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 3052.

3: gap of 100 bp
3: contig of 14451 bp in length
3: gap of 100 bp
7: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 9900 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute Center code: SC
Web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
                                                                                                                                                                                                                                           1147 RRRRRRRRRRRRRR 1127
                                                                                                                                                                                                                         307 AGAGAAAGGTCAGAGACAGAA 327
                                                                                                                                                                                                                                                                                                                                                                                                    BX855623.1 GI:39573499
                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3752:
18203:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34897:
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31202
34798
34898
                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                     RESULT 13
BX855623
                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with missequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; Sw., SWISSROT; Tr., TREMEL; Wp.; WORMPEP; Information on the WORMPEP database can be found at hother. Wormper Repeat names beginning 'Dr.' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr.' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr.' were identified by the Recon repeat discovery system (ZHI-Let information see http://www.brojects/D_rerio/fishmask.shtml Lorel: Lorel: is from a CHORI-211 BAC library

Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lorel: Lo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120237 AAGACAAATAACCACTCGATACAACTGAGTTGTGCAGAAGAGCATCTCTAAAAGCACAAC 120178
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                             Submitted (13-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 24, 2003 this sequence version replaced gi:28460278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK125521.1 GI:34531645
oligo capping; fis (full insert sequence).
Momo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAAGAATCAAAAGAAGCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 5; Length 188317;
Pred. No. 0.025;
0; Mismatches 55; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A218 bp mRNA linear
Homo sapiens cDNA FLJ43533 fis, clone PLACE7001544.
AK125521
                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                           Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                    Contact: zfish-help@sanger.ac.uk
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/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA.
/db_xref="taxon:7955"
/clone="CH211-202P1"
/clone_lib="CHOR1-211"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%;
59.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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AK125521/C
LOCUS
DEFINITION
ACCESSION
VERSION
XEYWORDS
SOURCE
ORGANISM
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Matches
AUTHORS
TITLE
JOURNAL
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                                                                                                                                           COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144171 ACATGAAACCTTGAGGCGGATGGCTACAGGGGAAAAGACCACATCTGTCGGCTAAGAA 144230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAAAAAAAGAAGCCCAAG 60
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                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:00210
fragment_chain:2"
103563. 107200
fragment chain:2"
fragment chain:2"
107301. 111003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149425. _152942

/note="assembly fragment:00098

fragment_chain;2"

153043. _164529

/note="assembly fragment:00529

fragment_chain;2"
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fragment_chain:3"
fr834. 177229
/note="assembly_fragment:00044"
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fragment_chain:2"
97311. .103462
                                                                                                                                                                                                                                                note="assembly_fragment:00117
ragment_chain:2"
11104. _128252
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12.1%; Score 49; DB 2;
Best Local Similarity 59.9%; Pred. No. 0.025;
Matches 82; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_fragment:00392
ragment_chain:3"
72505. _174733
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BX004780
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윱 ઠે a ઠે 셤 VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE

LOCUS RESULT 14 BX004780/c

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Kazusa-Kamatari, Kisazari, Chiba 292-0018, Japan Kazusa-Kamatari, Kisazari, Chiba 292-0018, Japan Kazusa-Kamatari, Kisazari, Chiba 292-0018, Japan Kazusa-Kamatari, Kisazari, Chiba 191-31-3375, Fax:81-438-52-396) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Hellx Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3202 gccirciacagacccaaggargccgarcccaaaagargararaaacrrcrargcc 3143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 CACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGGAC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 TICTGTTAGTAGGCCTTG---TICCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCC 401
                                                            Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Yukuzumi, Y., Fujimori, Y., Komiyama, M., Suqiyama, T., Irie, R., Otaski, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoro, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Wastsuo, K., Nakamura, Y., Sakine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Wurakawa, K., Kanebori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Maguho, Y., Nagai, K. and Isogai, T., Sugano, S., Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 CCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGGTATGAGGAACATTGACTCCCT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 9; Length 4218;
Pred. No. 0.075;
0; Mismatches 140; Indels
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Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
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                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 (bases 1 to 1045)

NIH-MGC http://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

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Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ucranism="Homo sapiens"
/mol_type="mRNA"
/db_xref="htmson:9606"
/clone="rikdgE:4109064"
/tissue_type="from acute myelogenous leukemia"
/tlasue_type="from acute myelogenous leukemia"
/tlast listid (ggccgcctcggco, site 2: sfil
/ggccattatggco; pouble-stranded cDNA was prepared from cell line RNA. 5 and 3 adaptors were used in cloning as follows: 5 adaptor sequence: 5 -CACGGCCATATGGCC-3 and 3 adaptor sequence: 5 -CACGGCCATATGGCC-3 and 5 -ATTCTAGAGGCCAGGCGCGACATG-dT(30)BN-3 (where B = A, C, of G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)

Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Http://mage.llnl.gov
Plate: LLCM993 row: a column: 01
Http://consortium/Collegion/Qualifiers
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10423 row: 1 column: 01
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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602414106F1 NIH_MGC_92 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                                                                             MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysPro---
                                                          ATGGGAAATTCTCTGCTGAGAGAAAAACAGGCGGCAGCAGAACACTCAAGAGATGCCTTGG 155
               -----LysLysGlyAsnProAspGluGluArgLysArg-----
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                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="manNa"
/db_xref="taxon:9606"
/clone="IMAGE:4522512"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/clone_lib="NIH_MGC_92"
/clone_lib="NIH_MGC_92"
/note="Organ; testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dr_primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                         cgi-bin/cluster.cgi?seq=CSODG007CB08QPl&cluster=1964.r. Contact Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODG007CB08QPl. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1964.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
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5', mAWA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12330 row: 1 column: 05
                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                         BM479887.1
                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. (CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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                                                                           quality sequence stop:
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/db_xref="taxon:9606"
/clone="IMAGE:5577364"
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/clone_state; Not of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembry of the contembraty."
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Percent Similarity: Best Local Similarity: US-10-005-907-2 (1-135) 141 AATGTGAGAATGCAAAGCCCCAAACAGAGAACATCCAGATGCTGGGATCACCATATCGCT 200 Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Louis Staudt, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium Eukaryota; Metazoa; Chordata; Craniata; V Mammalia; Eutheria; Primates; Catarrhini; 1 (Dases 1 to 1095) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Unpublished (1999) BG106563 602290373F1 NIH_MGC_85 Homo Homo sapiens BG106563 BG106563.1 mRNA sequence. Homo sapiens (human) MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysPro---CATGCCCGATCCCCAGAAGATGAATATGAACTTCTCATGCCTCAC GGGAACTCTGCTGAAGAGTACTATGAGAATGTTCCCTGCAAAGCTGAGAGACCCAGAGAG LeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArgGln 101 GlySerGluGluValCysTyrThrVallleAsnHis---IleProHisGlnArgSerSer GlnAspLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySer 62 GAAGGGTGTTTCTGCCTTCCATGGAAAAAAAATACTCATTTTTGAAAAAGAGG---CAAGAT 257 -----LysLysGlyAsnProAspGluGluArgLysArg---ATGGGAAATTCTCTGCTGAGAGAAAAACAGGCGGCAGCAGAACACTCAAGAGATGCCTTGG SerCys---ThrHisGluHisAspTyrGluValValPheProHis 135 PheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgProCys TACTCAGAGGAGCTGTGCTATACCCTCATCAATCATCGGGTTCTCTGTACAAGGCCATCA TCCCAAAACGAAAATGAAAGAATGTCATCTACTCCCATCCAGGACAATGTTGACCAGACC TCCTTGGGAGGAACTGAGACTGAGTATTCACTTCTACATATGCCTTCTACAGACCCCAGG 5.02e-0 169.50 51.61% 30.32% 23.71% x BM479887 (1-1039) GI:12600409 ------GlnGluMetThrThrPheGluArgLysLeuGlnAsp 42 02e-07 1095 Length: Matches: Conservative: Mismatches: Indels: Gaps: sapiens Craniata; Vertebrata; Catarrhini; Hominidae; mRNA line s cDNA clone Gene linear Collection (MGC) IMAGE: 4385178 Buteleostomi; ; Homo. (LLNIL) EST 30-JAN-2001 1 1 1 1 1 1 . υ 121 497 437 377 81 140 317 30

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                                                                                                                                                                                                                                                                                                                                                                                           43 GlnAspLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySer
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BF795688
BF795688.1
EST.
Homo sapiens
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PinGluMetThrThrPheGluArgLysLeuGlpAsp 42
                                                                                                                                                                                                                       PheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgProCys 121
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Note: this is a NTH_MGC Library."
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US-10-005-907-2 (1-135) x BF795688 (1-1124)
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Email: cgapbs-r@mail.nih.gov

Tissue procurement: Louis Staudt, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LIML at:

http://image.llnl.gov

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1 (bases 1 to 1124)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                           TCCCAAAACGAAAATGAAAGAATGTCATCTACTCCCATCCAGGACAATGTTGACCAGACC
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SerCys---ThrHisGluHisAspTyrGluValValPheProHis
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Note: this is a NIH_MGC Library."
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us-10-005-907-2.rst

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BM456595 1070 bp mRNA linear EST 05-FEB-2002 AGENCOURT_6409034 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5496261 5', mRNA sequence.
BM456595.1 GI:18505635
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                                                                                                                                                                                                                                                                                                                       100 ArgGlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArg 119
80 SerSerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysVal 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2002) 1 (2
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Note: this is a NIH_MGC Library."
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VERSION
KEYWORDS
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/lab host="lymphoma, call line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_88"
/note="Corgan: lymph, Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1:867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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(bases 1 to 1000)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information con be found through the I.M.A.G.E. Consortium/Link at:
http://inage.llnl.gov
Plate: LiAM12131 row: b column: 05
High quality sequence srop: 698.
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                   CATGCCCGATCCCCCAGAAGATGAATATGAACTTCTCATGCCTCAC
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/clone="IMAGE:5499556"
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1085)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CONA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://mage.llnl.gov
Plate: LLAMILISS row: d column: 24
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AGENCOURT 6407334 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5500391
5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 ArgGlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 CAAGATICCCAAAAGGAAATGAAAGAATGTCATCTACTCCATCCAAGACAATGTTGAC 301
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High quality sequence stop: 760.
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                                                                                                  US-10-005-907-2 (1-135) x BM455198 (1-1193)
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SAGNCOURT 6405645 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:5500141
5', mRNA sequence.
BM455198
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://lange.llnl.gov

Plate: LLAMI2134 row: j column: 14

High quality sequence stop: 592.
                                                                                                                                                                133 CCATCAGGGAACTCTGCTGAAGAGTACTATGAGAATGTTCCCTGCAAAAGCTGAGAGACCC 492
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      41 GlnAspGlnAspLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsn 60
                                                                                                                                                                                                                                                                                                    SerSerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysVal 99
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_68"
/note="Corgan: lymph, Vector: pCNV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_1:67 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                ------GlnGluMetThrPheGluArgLysLeu 40
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1193)
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EST 01-JUN-2000 mRNA sequence.
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1 (bases 1 to 683)
1 Hegde, P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.B., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon tumor
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
1. 508
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                        293 GAGAAIGTTCCCTGCAAAGCTGAGAGACCCAGAGAGTCCTTGGGAGGAACTGAGACTGAG
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Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Par: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 bp mRNA linear
BST375439 MAGE resequences, MAGH Homo sapiens CDNA,
AM962366
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                 /gene="GCET2"
/locus_tag="HCM1940"
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Plate: 187
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156.50
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L (bases 1 to 508)
Clark, A.G. (alanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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/lab.host="DH10B (phage-resistant)"
/clone lib="NIH MGC_85"
/note="lorgan: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1:867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Direct Submission Clargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                   GlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluVal
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genomic survey sequence.
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BQ214406
BQ214406.1 GI:20395806
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33
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33
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/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptsKm"
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Matches:
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/mol_type="mRNA"
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Query Match:
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AUTHORS
TITLE
JOURNAL
COMMENT
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BG024891 1041 bp mRNA linear EST 24-JAN-2001
G0275814F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGB:4363899 5',
mRNA sequence.
BG024891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 TyralaLeuLeuArgThrSerValSerArgProCysSerCys---ThrHisGluHisAsp 128
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/clone="INAGE:6070669"
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/lab_host="NHIOW [phage-resistant)"
/clone lib="WIH MGC 92"
/note="Organ: testis, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidarectionally; oligo-eff primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: ogapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Htp://image.lnll.gov

Right quality sequence start: 2
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 SerSerThrSerAsnGluAsnGluAsnGlySerGlySerGluGluValCysTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 GlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluVal
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228
339
339
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1. .1041
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/db xref="taxon:9606"
/clone="InAGE:4161899"
/tissue_type="lymbhoma, cell line"
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/lab host="DH10B (phage-resistant)"
/lone_lib="NHH0B (phage-resistant)"
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/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lymph; Vector: pCMV-sporte; primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 LeuThrArgLysValArgGlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArg 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GlnGluAsnGluAsnGlySerGlySerGluGluValCysTyrThrValIleAsnHis--- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluValSerSerThrSerAsn 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLys---- 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GCTGGGATCACCATATCGCTGAAGGGTGTTTCTGCCTTCCATGGCAAAAAATACTCATT
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488
35
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Matches:
Conservative:
Mismatches:
Indels:
High quality sequence stop: 541.
Location/Qualifiers
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Ab113404 Drosophil
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Aba83301 Human sec
Ach48612 Human sec
Ach48612 Human CDN
Ac76938 Human CNR
Ab132295 Human imm
Abx09875 N. mening
Abq46432 Oligonucl
Abq46433 Oligonucl
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Aba81529 N. mening
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                                         Rat gene
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Aca03930 c
Ada18223 P
Adb48220 Aai.60039 P
Aax84690 c
Abk47580 Abk47580 Abc49802 P
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Acd44612 P
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ADC30760
           Command line parameters:
-MODEL=frame+ p2n.model -DBV=xlp
-MODEL=frame+ p2n.model -DBV=xlp
-Q=/Cap21_/USPTO-epool_p/US10005907/runat_21042004_113753_11422/app_query.fasta_1.327
-Q=/Cap21_1/USPTO-epool_p/US10005907/runat_2104204_113753_11422/app_query.fasta_1.327
-DB=N Geneeq_29Gan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosmed2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LDCAL -CUTFMT=pc0 -NORM=ext -HEAPSIZE=500 -MINLENE=0 -MAXLENE=200000000
-USER=US10005907_@CGN 1 1_708 @runat_2104204 113753_11422 -NCFU=6 -ICPU=3
-NO_MMAP -LARAGOUERS -NEG_SCORES=0 -MALT -DSEBLOK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THERAES=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abn81319 Human mas
Acc9951 Human IRA
Ab199791 Human sec
Abx05108 Human sec
Ada56130 Gene enco
Ada39940 Human sec
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                    - núcleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Scoring table:

ö Weng Asundi V, Wang Z, Ma Y, Zhou P, Ghosh M, Wang D, M Haley-Vicente D, Drmanac RT;

WPI; 2003-371981/35 P-PSDB; ADC31731 New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer.

SEQ ID NO 842; 1185pp; English. Claim 1;

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC31089) and the polypeptides they encode (ADC30800-ADC3106). The invention also relates to mucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an enthod of detecting polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or and/or polypeptides of the invention. The invention methods for the identification of compounds that modulate the invention, methods for the identification of compounds that modulate the invention, methods for the identification of compounds that modulate the couring sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, and polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded by the contigs (ADC32627) and the polypeptides encoded for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases and cuttoff markers, and as food supplements. The present sequence represents a specifically and as food supplements. The present sequence of the ftp.wipo.int/pub/published_pct_sequences.

Sequence 667 BP; 216 A; 147 C; 154 G; 150 T; 0 U; 0 Other;

186 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAG 245 GGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCC 425 306 caagarcaagaraagaaaagccaagaagrrrcarccacrrcraarcaggaaaacgagar 365 21 LysGlyasnProAspGluGluArglysArgGlnGluMetThrThrPheGluArglysLeu 40 GlnAspGlnAspLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsn 60 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys 20 GlySerGlySerGluGluValCysTyrThrVallleAsnHisIleProHisGlnArgSer 6667 0 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: US-10-005-907-2 (1-135) x ADC30760 (1-667) 8.24e-76 715.00 100.00% 100.00% Score: Percent Similarity: Best Local Similarity: 41 61 Query Match: DB: ઠે ద ò g ò g ઠે

80

The invention relates to isolated nucleic acid (ABN81319-ABN81324), corresponding to genes differentially expressed in mast cells following activation or in patients with allergic hypersensitivity disease, [1] that encodes proteins (ABB77569-ABR77575) [11] or a protein fragment of [11] if at least 6 amino acids. [11] is useful for identifying binding partners. [1] or [11] is useful for identifying binding partners. (1) or [11] is useful for diagnosing or treating a disease state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma, urticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of [1] or [11]. A computer system, comprising a database containing information identifying the expression level in a tissue or at least one mast cell of [1], is useful for passenting information to identify the relative expression level of containing information and allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise 120 485 545 Human, mast cell; MC; antiallergic; antinflammatory; antiasthmatic; vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma; Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity. GlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg CysSerCysThrHisGluHisAspTyrGluValValPheProHis 135 TGTTCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCCACACAC 590 Human mast cell related gene MC1 SEQ ID NO 1. Claim 1; Page 95-97; 119pp; English. Location/Qualifiers Einstein R; E COM 08-DEC-2000; 2000US-0251835P. 14-MAR-2001; 2001US-0275479P. 28-MAR-2001; 2001US-0279115P. 02-APR-2001; 2001US-0280143P. ABN81319 standard; cDNA; 3762 07-DEC-2001; 2001WO-US046180. 25. .432 /*tag= a /product= ' (first entry) Nocka K, Pirozzi G, WPI; 2002-508560/54. P-PSDB; ABB77569. (UNIO) UCB SA. WO200246389-A2 30-AUG-2002 Homo sapiens. 13-JUN-2002 gene; ss. 101 121 546 ABN81319; 81 RESULT 2 ABN81319 ઠે 셤 ઠે

(II) is useful for identifying

monoclonal antibodies.

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SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
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                        agents that modulate expression of the protein or agents, such as agonists or antagonists. The agonists or antagonists are useful for modulating biological activity and function of (II) and thus are useful for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys
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                                                                                                                                                                                                                      Sequence 3762 BP; 1220 A; 672 C; 680 G; 1190 T; 0 U; 0 Other;
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ACC59924 to ACC59958 encode the human immune response associated proteins canti-HV, antialieragic, antianimal and than an immune response associated proteins canti-HV, antialieragic, antianimal antianaemic, antiparkinsonian, nootropic, anticanvulsant, antianteraics-cordic, antiaschmatic, antiparkinsonian, antianteraic, neprotropic, thyrominentic, neuroprotective, osceopathic, antiabetic, nepricorropic, thyrominentic, neuroprotective, osceopathic, antiatrhritic, antiparastici, antihelminthic, antipasoriatic, uropathic, ophthalmological, antirheumatic, haemostatic, antibacterial, uropathic, ophthalmological, antirheumatic, haemostatic, antibacterial, virucide, protocoacide and fungatice activities, and can be used in gene therapy. Human IRAP polymucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of IRAP, such as immune system disorders (e.g. Achime, gout, diabetes mellitus, glomerulonephritis, Good pasture's syndrome, gout, drawes' disease, Hashimoto's thyroiditis, conteoporosis, panchame, gout, cancel disorders (e.g. ranal tubular assistics) and multiple sclerosis, osteoarthritis, Sjogren's syndrome, uveitis, and epilepsy), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), muscle disorders (e.g. arteriosclerosis, contental retardation), muscle disorders (e.g. arteriosclerosis, contental retardation), muscle disorders (e.g. arteriosclerosis, contental retardation), muscle disorders (e.g. arteriosclerosis, charactolyosetias, polycythaemia vera, perivaysmal nocturnal charactoric, and anticontental disorders (e.g. arteriosclerosis, charactolyosetias, polycythaemia vera, paroxysmal nocturnal charactoric, and anticontental disorders (e.g. arteriosclerosis, charactolyosetias, orthography, paroxysmal nocturnal fundal disorders (e.g. arteriosclerosis, charactolyosetias), or viral, bacterial, fungal, parastitic, contental disorders (e.g. arteriosclerosis, charactolyosetias), or viral, bacterial, fungal, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human immune response associated proteins and polynucleotides, useful for diagnosing, treating or preventing immune system disorders, e.g. AIDS or anemia, cell proliferative disorders, e.g. cancer, or neurological
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Yue H;
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onchell CD;
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/product= "IRAP-28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 208; 213pp; English.
                                                                                                                                                                                  2001US-0324034P.
2001US-0327395P.
2001US-0342810P.
2001US-034468P.
2001US-0332140P.
2001US-0332140P.
2001US-033740P.
2002US-0347693P.
2002US-036279P.
                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2002; 2002US-036494P.
10-MAY-2002; 2002US-0379876P.
11-JUN-2002; 2002US-0388180P.
                                                                                                                                            19-SEP-2002; 2002WO-US029979
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P-PSDB; ABR43232.
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21-NOV-2001;
07-DEC-2001;
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264

144

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20 84 204

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Sequence 732 BP; 213 A; 178 C; 178 G; 163 T; 0 U; 0 Other;

helminthic infections

Length: Matches: Conservative: Mismatches:

1.28e-10 169.50 51.61% 30.32%

Percent Similarity: Best Local Similarity:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; gene; secretory protein; secretory polynucleotides; SPTM; SPTM-related dieease; somatic gene therapy; germiline gene therapy; severaline protection; fungal parasite; protection; fungal parasite; protection; neurological disorder; parkinson's disease; motor neuron disorder; prion diseases; multiple sclerosis; meningitis; abscess; prion diseases; cerebral palsy; dermatcomyositis; polymyositis; myopathy; myasthenia gravis; mental disorder; Tourette's syndrome.
                                                                                                                                                                                              111 TCCCAAAAAGAAAAAGAAATGTCATCTACTCCCATCCAGGACAATGTTGACCAGACC 370
                                                                                                                                                                                                                                        371 TACTCAGAGGAGCTGTGCTATACCTCATCAATCATCGGGTTCTCTGTACAAGGCCATCA 430
                                                                                                                                                                                                                                                                     82 LeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArgGln 101
                                                                                                                                                                                                                                                                                  102 PheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgProCys 121
                                                                                                                                                                                                                                                                                                                                    491 TCCTTGGGAGGAACTGAGACTGAGTATTCACTTCTACATATGCCTTCTACAGACCCCAGG 550
                                                                                                                                                          254 GAAGGGTGTTTCTGCCTTCCATGGAAAAAAAATACTCATTTTTGAAAAGAGG---CAAGAT 310
                                                                       134 Ariescalahrererischichschanananaschescescanschanenererangenschies 193
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                                                                                                                                                                                                                           GlySerGluGluValCysTyrThrValIleAsnHis---IleProHisGlnArgSerSer
                                                                                                            ----GlnGluMetThrThrPheGluArgLysLeuGlnAsp
                                                   MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysPro-
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22
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2000US-0229751P.
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The invention comprises the amino acid and coding sequences of human screenory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for tracting a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in parasites and protection against intracellular parasites (e.g. fungal parasites and protozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. multiple sclerosis), meningitis, abscesses, prion diseases (e.g. multiple sclerosis), meningitis, abscesses, prion diseases, cerebral palsy, neurological disorders, pertipheral nervous system disorders, and mental disorders (e.g. Tourette's syndrome). CDNA sequences ABL99746 - ABL99929 represent human secretory polynucleotides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL; Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; Momlyama MG, Bradley DL, Rohatej SD, Harris B, Roseberry AM; Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A; Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
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2000US-0230599P.
2000US-0230610P.
2000US-0230864P.
2000US-0230865P.
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2000US-0230990P.
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06.SEP-2000;
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                                                                                                                                                                  GlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro 120
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                                                                                             SerGlySerGluGluValCysTyrThrValIleAsnHis---IleProHisGlnArgSer
                                    GlnAspLysLysSerGlnGluValSerSerThrSer---AsnGlnGluAsnGluAsnGly
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                         --- GlnGluMetThrThrPheGluArgLysLeuGlnAsp
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Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
Wang D, Drmanac RT;
                                                                                                                                                                                                                AGGCATGCCCGATCCCCAGAAGATGAATATGAACTTTTCATGCCTCAC 1560
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Yang Y, Ma
T, Wang J,
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atopic dermatitis.
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Wehrman T,
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The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, medical imaging, identification of mutations

Claim 1, SEQ ID NO 123; 235pp; English.

disorders, and infections.

New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; osciptive disorder; schlarophrenia; prosetat; observed; schlarophrenia; prosetate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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566 GAGTATTCACTTCTACATATGCCTTCTACAGACCCCAGGCATGCCCCGATCCCCAGAAGAT 625
responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or amellorating medical conditions, such as cancer, neurodegenzative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone desenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABX04986-ABX05511 represent human polymucleotides of the invention. Note: The sequence data for this patent is not represented in the Buxopean Patent Office
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Query Match:
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This sequence represents a nucleic acid molecule which encodes a secreted detailed in the descriptor line. The gene can be used too generate fusion proteins the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Rc portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907, amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
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752 AAGGAGGACGGGAGGCTGTGTCTCAGCTGCAGACGCCCAAGTTTCACTCT 811
                                                                                                                                                                                                                                                                                     1, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuleuArglysLeuSerCysleuGlyGluAsnGlnLyslysProlyslysGlyAsnPro 24
                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 LysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 346; 484pp; English.
                                                            98US-007856EP.
98US-0078573P.
98US-0078574P.
98US-0078577P.
98US-0078578P.
98US-0078573P.
98US-0078531P.
98US-0080312P.
                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                98US-0078563P
                 99WO-US005804
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                  18-MAR-1999;
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19-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CRS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatis, cerebroprotective; neuroprotective; nootropis; cardiovascular; antiarteriosclerotis; gene therapy; human secreted protein; immune disorder; inflammation; respiratory disorder; cancer; CNS disorder; neurodegenerative disorders; inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy; multiple sclerosis; ischemic brain injury; Parkinson's disease; and Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic biology; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.
                              812 GAATCTCTATCTAACCCTTCCTCTTTTGCTCCCCGGGTACGAGAAGTAGAGTCTACT
                                                                       -----GluAsnileAspSerLeuThrArgLysValArgGlnPheArgGlu---
                                                                                                         872 CCTATGATAATGGAGAACATCCAGGAGCTCATTCGATCAGCCCCAGGAAATAGATGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene encoding human secreted protein #309.
                                                                                                                                                                                                                                                     992 CTGCCCACACAGAGCCTTGCTGGTGC 1018
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---SerieuSerSerAsnAspAspGlyTyr-
                                                                                                                                                                                                                             115 ThrSerValSerArgProCygSerCyg
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                      20-NOV-2003 (first entry)
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c disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephratitis or Crohn's disease), respiratory disorders (e.g. authma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative c disorders (e.g. parkinson's disease). The disease, and cardiovascular disorders (e.g. atherosclerosis or uyocarditis). The polymucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals con antisense DNA or RNA, in gene therapy, for identifying individuals con antisense DNA or RNA, in gene therapy, for identifying individuals condium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for creating or preventing neural disorders, immune system disorders, censal, proliferative and/or cancerous diseases. This sequence corresponds to a gene encoding one of the polypeptide of the invention. Note: The cancer data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.

Squence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.:
Pred. No.:
98.00
Matches:
36
Percent Similarity:
13.71\$
Gaps:
13.71\$
Mismatches:
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US-10-005-907-2 (1-135) x ADA56130 (1-1892)

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                                                                                                            45 LysLysSerGinGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySer 64
LeuleuArglysLeuSerCysleuGlyGluAsnGlnLysLysProLysLysGlyAsnPro 24
                                                                                                                             ::::: |||||||| |||::: caggaagaagaagaagaagaagaagaaaagagacaggaact
                                                                                                                                                                                    25 AspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAsp
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                                                                                                                                                                                                                        ---SerLeuSerSerAsnAspAspGlyTyr----------
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ADA39940 standard; cDNA; 1892

RESULT 8 ADA39940 20-NOV-2003 (first entry)

ADA39940;

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The invention relates to novel genes ADA39629-ADA40565 and proteins ADA40566-ADA41501 for human secreted proteins, useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind to the polypeptide are disposed or preventing cancer or other hyperproliferative disposed. The polypeptides and nucleic adjanostic or pharmaceutical composition for disposing or treating cancer or other hyperproliferative disorders or other hyperproliferative disorders including neoplasms, autoimmune of sporders (e.g. diabetes, thematofa arthritis, systemic lupus or other hyperproliferative disorders including neoplasms, autoimmune disorders (e.g. diabetes, thematofa arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or hematological disorders (e.g. anaemia, thrombocytopenia), allergic reactions including asthma or eczema, thrombocytopenia), allergic reactions including asthma or eczema, thrombocytopenia), allergic reactions including asthma or eczema, thrombocytopenia, allergic reactions including asthma or eczema, thrombocytopenia, allergic reactions including asthma or eczema, thrombocytopenia, allergic reactions including asthma or eczema, thrombocytopenia, allergic reactions including multiple, or ordivaters (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial, fungation or disposed or parkinson's disease), cardiovascular disorders (e.g. atherosche identification, radiation hybrid mapping or long-crange restriction mapping, as molecular weight markers, or as the setting and multiple and multiple probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification or disposed in munohistochemistry assays. Note: The sequence data for other part direction in electronic format directly from NIPO at
                                     Human; secreted protein; cancer; hyperproliferative disorder; rheumatoid arthritis; autoimmune disorder; haematopoietic disorder; anaemia; allergic reaction; asthma; cardivosscular disorder; wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepacotropic; autidiabetic; antiinflammatory; vulnerary; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating cancer or other hyperproliferative disorder, asthma, allergies or AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtained in electronic format directly fr
ftp.wipo.int/pub/published_pct_sequences.
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Human secreted protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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Pred. No.:
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                                                                                                                                                                                                              871
                                                                                                                                                                                                                                   ------GluasnileAspSerieuThrArgLysValArgGlnPheArgGlu--- 104
                                                                                                                                                                                                                                                                             ------ArgSerGluThrGluTyrAlaLeuLeuArg 114
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932 AATGAAATATATGATGAGAACCCTACTGGGAGAAACCCTGGCAGG 991
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                                                                                                                                                                                                                                                       872 CCTATGATAATGGAGAACATCCAGGAGCTCATTCGATCAGCCCAGGAAATAGATGAAATG 931
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                                                                                                      LysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySer 64
                                                                                                                     LeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLysLysGlyAsnPro
                                                             25 AspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAsp
                                                                                                                                               Gluglu-------ValCysTyrThrValIleAsnHisIleProHisGlnArgSer
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                                                                                                                                                                                          ---SerieuSerSerAsnAspAspGlyTyr----
                                                                                                                                                                                                                                                                                                                                           CIGCCCCACACAGAGCCTTGCTGGTGC 1018
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US-10-005-907-2 (1-135) x ADA39940 (1-1892)
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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P-PSDB; ADC74193.
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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemotolegic disorder such as anaemia, autoimmune disorders useful for preparing a composition for diagnosing or treating a haemotolegic disorder such as anaemia, autoimmune disorders useful arthritis, inflammation, Grave's disease, clabetes, systemic lupus erythematosus or glomerulonephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperpoliferative disorders including care therrosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during gene the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA of
New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 CTCCTACAATCCTCCTTGTCCCTGGGAAGCCAGGAGCAAGCGCCAGAGCACAAAGCAGGAG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LeuleuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLysLysGlyAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 LysLysSerGlnGluValSerSerThrSerAsnGlnAsnGluAsnGlySerGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GluGlu------ValCysTyrThrValIleAsnHisIleProHisGlnArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  752 AAGGAGGGAGGGTGTGTCTCAGCTGCAGACACACTCAGAGCCCCAAGTTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      812 GAATCTCTATCTTCTAACCCTTCCTCTTTTGCTCCCCGGGTACGAGTAGAGTCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SerLeuSerSerAsnAspAspGlyTyr--------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GluAsnIleAspSerLeuThrArgLysValArgGlnPheArgGlu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                        Claim 27; SEQ ID NO 211; 2272pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 ThrSerValSerArgProCysSerCys 123
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ID ADD37623 standard; cDNA; 1892
XX
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98.00
38.26%
24.16%
13.71%
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Best Local Similarity:
                                                                                            atherosclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention.
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DB:
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83

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104

-----GluAsnIleAspSerLeuThrArgLysValArgGlnPheArgGlu---

-----ArgSerGluThrGluTyrAlaLeuLeuArg

1018

ВР

ThrSerValSerArgProCysSerCys 123

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812 GAATCTCTATCTTTAACCCTTCCTCTTTTGCTCCCCCGGGTACGAAGTAGAGTCTACT 871
                                                                                                                                                                                                                                                   872 ccranganaanggagaacanccaggagchcanncgancagcccaggaaanagangaaag 931
                                                                                                                                                                                                                                                                                                                   932 AATGAAATATATGATGATGAGAACTCCTACTGGAGAAACCAAAACCCTGGCAGCCTCCTGCAG 991
65 GluGlu-------ValCysTyrThrVallleAsnHisIleProHisGlnArgSer
                                                                                                                 ...|||
752 AAGGAGGACGGGAGGCTGTCTCAGCTGCAGACTCAGAGCCCAAGTTTCACTCT
                              45 LysLysSerGlnGluValSerSerThrSerAsnGluAsnGluAsnGlySerGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; ds; gene; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                           81 ---SerLeuSerSerAsnAspAspGlyTyr---
                                                                                                                                                                                                                                                                                                                                                                                992 crecccacacacaccitricitecresic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat gene U02506, SEQ ID NO 7951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE62022 standard; DNA; 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the protein. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind are useful for preparing a diagnostic or antagonists that bind are useful for preparing a diagnostic or natagonists that bind are useful for treating allergic or asthmatic disorders. The polypeptide is also useful for identifying a binding partner by contacting the polypeptide with a binding partner, and determining whether the binding partner increases or decreases the activity of the polypeptide. The polypeptides and nucleic acid molecules are also useful for detecting, preventing, diagnosting, proposticating, reating or ameliorating inflammatory disorders neoplastic diseases, wound healing and disorders of epithelial cell proliferation, immune disorders, cardiovascular disorders, blood-related disorders, infectious diseases, endocrine disorders, or gastrointestinal disorders. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction probes. The polypeptides and antibodies are useful for providing immunohighted probes for differential identification or diagnostic immunohighted probes for differential identification of the tissues immunohighted.
                                                                                           human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numunohistochemistry assays. The present sequence represents a human secreted protein encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                preparing a diagnostic or pharmaceutical composition for diagnosing treating allergic or asthmatic disorders, or related immediate hypersensitivity disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to an isolated polypeptide or human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
                                                                Human secreted protein encoding sequence #105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; SEQ ID NO 105; 1323pp; English.
                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                         19-MAR-2002; 2002WO-US008279.
                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-140218/13.
                                                                                                                                                                            WO200290526-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1892
                                15-JAN-2004
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                          14-NOV-2002
 ADD37623;
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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host call comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to parform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence
                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
Costigan M;
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 1017pp; English.
    Befort K,
    D'urso D,
                                                                                   WPI; 2003-268312/26
GENBANK; U02506.
    Woolf C,
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25 AspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAsp 44

LeuleuArgLysLeuSerCysleuGlyGluAsnGlnLysLysProLysLysGlyAsnPro 24

Length:
Matches:
Conservative:
Mismatches:
Indels:

0.156 98.00 38.26% 24.16% 13.71%

Percent Similarity: Best Local Similarity:

Best Local S: Query Match:

Alignment Scores: Pred. No.:

Gaps:

US-10-005-907-2 (1-135) x ADD37623 (1-1892)

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that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and (e.g. spinal segmental nerve injury (CMI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the sequence data for this patent did not form part of the printed secification, but was obtained in electronic form directly from WIPO at fib. Whypolished_pot_sequences.
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Sequence 584 BP; 247 A; 75 C; 175 G; 87 T; 0 U; 0 Other;

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13 GlyGluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGlu
232
232
133
133
133
133
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                     Gaps:
                                                  US-10-005-907-2 (1-135) x ADE62022 (1-584)
0.0495
96.50
46.72%
26.23%
13.50%
               Percent Similarity:
Best Local Similarity:
Query Match:
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344 TCTTITCTGTCTCACCTI-----TCCCTTCCGTCACTTGGACCTCAA 388
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                                                                                                                                                                                                                                                                                           448
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                                                                                                                                                                                                                                                                                                                                                         508
                           32
                                                              22
                                                                                                                             69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisense oligonucleotide; c-trk; ds.
                                                                                                                                                                                                                                                                                         449 CCGGGAGCAGCGTTCTCCAAAGTCAAATTAGACTGTTCTCTCTGAGCCTGTACTTCACCA
                                                           33 MetThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluValSerSer
                                                                                          ThrSer-----AsnGlnGluAsnGluAsnGlySerGlySerGluGluValCysTyr
                                                                                                                                                                                         70 ThrVallleAsnHisIleProHisGlnArgSerSerLeuSerSerAsnAspAspGlyTyr
                                                                                                                                                                                                                                                          90 GluAsnIleAspSerieuThrArglysValArgGlnPheArgGluArgSerGluThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV20445 standard; DNA; 2301 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human c-trk oncogene.
                                                                                                                                                                                                                                                                                                                                                                                       126 uHis 127
                                                                                                                                                                                                                                                                                                                                                                                                                      509 GCAC 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV20445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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ID AAV2
XC
AC AAV2
XX
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DT 17-J
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DE Huma
XX
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Huma
XW
ANM
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96 53 317 GAGCGCCTCCAGCGAGAAGTTGAGGGAGAAAAGGCGGGGCCCCGGGAACAGGCTGAGGCTGAG

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137 GAGGAGCAGGÁGCAGGÁGGAGCAGGAGGÁGAGÁGAGGCTGCAACGCCGAGCGGAGGAGGAGCC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AspSerLeuThrArgLysVal -----ArgGlnPheArgGluArgSerGluThrGlu 109
                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a composition which comprises two antisense oligonuclectides. The first oligonuclectide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonuclectide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ers, c-fcs, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin D1, PML/RAR alpha, AMLI/MTG9, EZA/prl and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonuclectides has synergistically enhanced ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGluMet 33
                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an oncogene from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 ThrThrPheGluArgLysLeuGlnAspGlnAspLysSerGlnGluValSerSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 AGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCAĆĆACCATĆGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 HislleProHisGlnArgSerSerLeuSerSerAsn---AspAspGlyTyrGluAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 SerAsnGluAsnGluAsnGlySerGlySerGluGluValCys------
                                                                                                                                                                                                                                                                       Anticancer composition comprising two anti-sense oligo:nucleotide(s) targetting cytoplasmic and nuclear oncogene(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2301 BP; 545 A; 568 C; 785 G; 403 T; 0 U; 0 Other;
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224
324
344
344
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                          Claim 1; Col 99-102; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibit growth of cancer cells
                                                                                                                                                                     UYJE-) UNIV JEFFERSON THOMAS
                                                                                                    94US-00306691.
                                                                                                                                    94US-00306691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.35
96.00
41.41%
22.66%
                                                                                                                                                                                                      Calabretta B, Skorski T;
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                                                                                                                                                                                                                                        WPI; 1998-229882/20.
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Best Local Similarity:
 Homo sapiens.
                                                                                                  LS-SEP-1994;
                                                                                                                                    .5-SEP-1994;
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                                US5734039-A.
                                                                   31-MAR-1998
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New complex of a NLK1 protein and a NLK1 protein-interacting protein, useful for treating cancer, hyperproliferative disorder, neurodegenerative disorder, cardiomyopathies, viral infections and metabolic disorders.
                                                                       NIK1 Interacting Protein; Trk oncogene A; TrkA; protein complex; cytostatic; antiviral; neuroprotective; cardiant; ss.
                                                                                                                                                                                                                                                                                                                      Example 1; Page 126-130; 172pp; English.
                                                       Human Trk oncogene A coding sequence
                                                                                                                 Location/Qualifiers
233. .2158
/*tag= a
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                                                                                                                                                                                                                                     Yang
        AAA09303 standard; DNA; 2301 BP
                                                                                                                                                                                   99WO-US023314.
                                                                                                                                                                                                    98US-00167206
                                        (first entry)
                                                                                                                                                                                                                                    Nandabalan K, Schulz VP,
                                                                                                                                                                                                                    (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                     WPI; 2000-303742/26.
P-PSDB; AAY92331.
                                                                                                                                                   WO200020448-A2.
                                                                                                                                                                                  06-OCT-1999;
                                                                                                                                                                                                    06-OCT-1998;
                                                                                                 Homo sapiens
                                       10-AUG-2000
                                                                                                                                                                    13-APR-2000.
                       AAA09303;
AAA09303
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AAA09303-09 were isolated in a modified yeast two hybrid system using NIKI protein as "bait". These are known sequences which encode NIKI interacting proteins. The invention concerns purified complexes of a NIKI protein and a NIKI protein-interacting protein, where the interacting protein is chosen from TrkA, protein phosphatase lalpha, 14-3-3epsilon, alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2, IP-3, IP-4, or IP-5. NIKI (also referred to as Nak2) is a human homologue of the Aspergillus nidulans mitotic regulator, NIMA kinase. NIKI is a serinefthreonine-specific kinase and is thought to play a key role in call-cycle events leading to the onset of mitosis. The complexes, their derivatives and NIKI or NIKI-IP protein and DNA sequences, etc. are useful for treating or preventing a disease or disorder involving caberrant levels of the complex or protein. Such disorders include cancer, hyperproliferative disorders, neurodegenerative disorders cardiomyopathies, viral infections and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2301 BP; 545 A; 568 C; 785 G; 403 T; 0 U; 0 Other;
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Best Local Similari
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14 GluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGluMet 33 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-10-005-907-2 (1-135) x AAA09303 (1-2301) 41.41% 22.66% 13.43%

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Sequence 1824 BP; 500 A; 591 C; 493 G; 240 T; 0 U; 0 Other;

316 136 137 GAGGAGCÁGGÁGCAGGÁGGAGCAGGAGGÁGAGGÁGGCTGCAACGCCGAGCGGAGGAGG 196 197 AGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAG 256 93 AspSerieuThrArgLysVal-----ArgGlnPheArgGluArgSerGluThrGlu 109 , B 73 92 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in alucidating cell signalling and cell-cell interactions in higher elevaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-AB130511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB27373-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions. --TyrThrVallleAsn 74 HislleProHisGlnArgSerSerLeuSerSerAsn---AspAspGlyTyrGluAsnIle 34 ThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluValSerSerThr Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster genomic polynucleotide SEQ ID NO 33958. Claim 1; SEQ ID NO 33958; 21pp + Sequence Listing; English. 54 SerAsnGlnGluAsnGluAsnGlySerGlySerGluGluValCys----Myers EW 110 TyralaLeuLeuArgThrSerVal 117 377 GTGGCCTCCTTGAACCGTAGGATC 400 ABL27495 standard; DNA; 1824 BP Li PWD, 23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. 26-MAR-2002 (first entry) pharmaceutical; gene; ds. Drosophila melanogaster. Venter JC, Adams M; WPI; 2001-656860/75. (PEKE) PE CORP NY WO200171042-A2. 27-SEP-2001 69 ABL27495; RESULT 14 ABL2749 g ò ሯ 셤 ठ 셤 ठ 셤 ઠે 셤

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                                                                                                                                                                GlySerGlu-------GluValCysTyrThrValIleAsnHisIleProHis
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23-AUG-2000; 2000US-00649167.
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                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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Alignment Scores:
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCK) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed carriers. (I) is useful in gene therapy techniques to restore normal activity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a crivity of (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and of its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in disqual for generating sequences have application of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. Asset197-Aas94564 represent novel human diagnostic codings sequences. Asset4197-Aas94564 represent novel human diagnostic coding sequences. Asset4197-Aas94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the wind sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 GAAGAAGAAGAAGAAGAAGGACTATCAATCAAGTATATGACAAGCACAAAGACCCTT 390
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|TCAGACATCAACGGATTTGAAAA-ATTACTTCCAGTACACCCTATTTTAGCAGTACTAGA
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                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Matches:
Conservative:
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                   WPI; 2001-639362/73.
P-PSDB; ABG06966.
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Search completed: April 22, 2004, 17:20:13 Job time : 360 secs

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Sequence 1, Application US/10005907
Publication No. US20030166881A1
APDLICANT: Union Chimique Belge, S.A.
APPLICANT: Union Chimique Belge, S.A.
APPLICANT: No. US20030166881Alka, Karl
APPLICANT: Piozzi, Gregory
APPLICANT: Binstein, Richard
TITLE OF INVENTION: ACTIVATION
FILE OF INVENTION: ACTIVATION
FILE REFERENCE: 053529-5005
CURRENT APPLICATION NUMBER: US/10/005,907
CURRENT APPLICATION NUMBER: US/10/005,907
CURRENT APPLICATION NUMBER: US/10/005,907
CURRENT APPLICATION NUMBER: DOI:112-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23224, A Sequence 3, Appli Sequence 17, Appl Sequence 67, Appl Sequence 54, Appl Sequence 10857, A Sequence 11, Appl Sequence 53, Appl Sequence 53, Appl Sequence 33, Appl Sequence 33, Appl
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         SEQ ID NO 1
LENGTH: 3762
TYPE: DNA
ORGANISM: Homo sapiens
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-DE=CORD 1/USFTO spool p/US10005907/runat_21042004_113756_11532/app_query.fasta_1.327
-DE=Published Applications NA -QFNT=fasta_P -SUFFIX=rnpb -MINMATGH=0.1
-LOOPEL-0 -LOOPEXT=0 -UNITE=bits -START=1 -END=1 -MATRIX=blosun62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=ECT -THR MAX=10
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-NORD-6 -ICDU=3 -NO MMAP -LARGEOURRY NEG SCORES=0 -WAIT -DSPBLOGR=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOF=10 -XGAPO
                                                                                                                            April 22, 2004, 17:57:48 ; Search time 334 Seconds (without alignments) 1822.349 Million cell updates/sec
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1. \(\cgn2_6\)\pubodata/2\)\pubpna/USO7_PUBCOMB.seq:*

2. \(\cgn2_6\)\pubodata/2\)\pubpna/USO7_NBW_PUB.seq:*

3. \(\cgn2_6\)\pubodata/2\)\pubpna/USO6_NBW_PUB.seq:*

4. \(\cgn2_6\)\pubodata/2\)\pubpna/USO6_PUBCOMB.seq:*

5. \(\cgn2_6\)\pubodata/2\)\pubpna/USO6_PUBCOMB.seq:*

6. \(\cgn2_6\)\pubodata/2\)\pubpna/USO8_NBW_PUB.seq:*

7. \(\cgn2_6\)\pubodata/2\)\pubpna/USO8_NBW_PUB.seq:*

8. \(\cgn2_6\)\pubodata/2\)\pubpna/USO8_NBW_PUB.seq:*

9. \(\cgn2_6\)\pubodata/2\)\pubpna/USO8_PUBCOMB.seq:*

10. \(\cgn2_6\)\pubodata/2\)\pubpna/USO9_NBW_PUB.seq:*

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12. \(\cgn2_6\)\pubodata/2\)\pubpna/USO9_NBW_PUB.seq:*

13. \(\cgn2_6\)\pubodata/2\)\pubpna/USO9_NBW_PUB.seq:*

14. \(\cgn2_6\)\pubodata/2\)\pubpna/USO9_NBW_PUB.seq:*

15. \(\cgn2_6\)\pubodata/2\)\pubpna/USO9_NBW_PUB.seq:*

16. \(\cgn2_6\)\pubodata/2\)\pubpna/USO9_NBW_PUB.seq:*

17. \(\cgn2_6\)\pubodata/2\)\pubpna/USO0_NBW_PUB.seq:*

18. \(\cgn2_6\)\pubodata/2\)\pubpna/USO0_NBW_PUB.seq:*

19. \(\cgn2_6\)\pubodata/2\)\pubpna/USO0_NBW_PUB.seq:*

19. \(\cgn2_6\)\pubodata/2\)\pubpna/USO0_NBW_PUB.seq:*

19. \(\cgn2_6\)\pubodata/2\)\pubpna/USO0_NBW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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FRICK APPLICATION NO. US20030065139A1

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PZ0.7PH Human Secreted proteins
FILE REFERENCE: PZ0.7PH Human Secreted proteins
FILE REFERENCE: PZ0.7PH Human Secreted proteins
FILE REFERENCE: PZ0.7PH Human Secreted proteins
FILE REFERENCE: PZ0.7PH Human Secreted proteins
FILE REFERENCE: PZ0.7PH J.7

FILE REFERENCE: PZ0.7PH J.7

FRIOR FILING DATE: 1999-09-17

FRIOR FILING DATE: 1999-03-19

FRIOR APPLICATION NUMBER: 60/078,576

FRIOR FILING DATE: 1998-03-19

FRIOR APPLICATION NUMBER: 60/078,573

FRIOR FILING DATE: 1998-03-19

FRIOR FILING DATE: 1998-03-19

FRIOR FILING DATE: 1998-03-19

FRIOR FILING DATE: 1998-03-19

FRIOR APPLICATION NUMBER: 60/078,579

FRIOR FILING DATE: 1998-03-19

FRIOR APPLICATION NUMBER: 60/078,579

FRIOR FILING DATE: 1998-03-19

FRIOR APPLICATION NUMBER: 60/078,579

FRIOR APPLICATION NUMBER: 60/080,314

FRIOR FILING DATE: 1998-03-19

FRIOR APPLICATION NUMBER: 60/080,314
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Best Local Similarity:
Query Match:
DB:
                                ; SEQ ID NO 90
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: HOMO 8
US-10-653-595-90
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19 Prior Application data removed - See File Wrapper or PALM.
PF SEQ ID NOS: 470
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TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P20207PGI
CURRENT FILING DATE: 2003-09-03
FRIOR APPLICATION NUMBER: US /10/653,595
FRIOR APPLICATION NUMBER: US 09/397945
FRIOR FILING DATE: 1999-09-17
FRIOR FILING DATE: 1999-03-18
FRIOR FILING DATE: 1998-03-19
FRIOR FILING DATE: 1998-03-19
FRIOR FILING DATE: 1998-03-19
FRIOR FILING DATE: 1998-03-19
FRIOR APPLICATION NUMBER: 60/078,576
FRIOR FILING DATE: 1998-03-19
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FRIOR APPLICATION NUMBER: 60/080,314
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Publication No. US20040048304A1
GENERAL INFORMATION:
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; OTHER INFORMATION:
US-10-005-907-1
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Publication No. US20030087412A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Schulz, Vincent P.
APPLICANT: Yang, Meija
TITLE OF INVENTION: NIXI PROTEIN AND NIXI PROTEIN COMPLEXES
FILE REPERENCE: 15966-521 NIXI protein complexes
CURRENT APPLICATION NUMBER: US/10/242,943
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PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FLIJNG DATE: 1998-04-01
PRIOR PLIJNG DATE: 1998-04-01
PRIOR PELING DATE: 1998-03-19
PRIOR PELING DATE: 1998-03-19
PRIOR PILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 90
LENGTH: 1892
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ORGANISM: Homo sapiens
US-09-397-945-90
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Shou Yihua
APPLICANT: Shou Yihua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53223)B
CURRENT PILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 8559
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OTHER INFORMATION: Clone ID: PAT_MRT3847_107747C.1
                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US/09/167,206
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 GIGGCCTCCTTGAACCGTAGGAIC 400
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41.41%
22.66%
13.43%
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (233)
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Pred. No.:
                                                                                                            LENGTH: 2301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54, Application US/10115831
; Publication No. US2030219743A1
; Publication No. US2030219743A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tang, Y. Tom
; APPLICANT: Bendi, Chenghua
; APPLICANT: Ren, Reiyan
; APPLICANT: Branca, Radoje T.
; TILE OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
; TILE OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
; TILE OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
; TILE OF INVENTION: No. US20030219743A1e1
; TILE OF INVENTION: 1920192ADIV
; CURRENT PRILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/667,298
; PRIOR APPLICATION NUMBER: 09/667,298
; PRIOR APPLICATION NUMBER: 09/667,298
; PRIOR PLING DATE: 2000-09-22
; PRIOR PLING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 54
; LENGHH: 6324
                                                                                                                                             AsnTyrLeuLeuArgLysLeuSerCysLeu---GlyGluAsnGln--
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Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
US-10-424-599-8569
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; LOCATION: (1)
US-10-115-831-54
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Pred. No.:
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US-10-115-831-54
                        Alignment Scores:
Pred. No.:
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                                                                                                                                                         397 GAGGAGATCGAGGAGGAGGATGAGGACGATGAGGATGGAGAAGATGAA
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                                                                                                                                                                                                                                                                                                                       517 ATGAATTGTCACAAT----ACTCGAATAATGCAAGACACAGAAAAGGATGATAACAAT
                                                                                                                      34 ThrThrPheGluArgLysLeuGluAspGluAspLysLysSerGlnGluValSerSerThr
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Sequence 22, Application US/10263929;
Publication No. US20040067535A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Alzheimer's Disease Linked Genes
FILE REFERENCE: LSD-07417 US/10/263,929
CURRENT APPLICATION WUMBER: 2002-10-03
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
LENGTH: 2862
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Matches:
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US-10-005-907-2 (1-135) x US-10-115-831-54 (1-6324)
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US-10-263-929-22
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595 GAGTCGTCCTCAGAATTACTTTCATTTGGATTCTCTTCAAAGAAGCTGAAA 654
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                                                                                                                                                  sequence 1552, Application US/10342887

publication No. U520040058340Al

genemace 1552, Application US/10342887

publication No. U520040058340Al

genemace 1552, Application No. U520040058340Al

genemace 1552, Applicant: Dai, Hongyue

APPLICANT: Linaley, Peter S.

APPLICANT: Mao, Mao, Mao, Mac, Marc, J.

APPLICANT: Roberts, Christopher J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Van de Vijver, Marc J.

APPLICANT: Bernards, Rene

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

TITLE OF INVENTION Diagnosis and Prognosis of Breast Cancer Patients

TURREYT FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: 10/112, 118

PRIOR PILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 5552

LEMOTH: $109
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US-10-342-887-1552
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US-10-172-118-1552
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                                                                                          APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Inhaley, Peter
APPLICANT: Mao, Mao.
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArg 119
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-0068
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 014965
DATABASE ENTRY DATE: 2001-06-18
1552, Application US/10172118
on No. US20030224374A1
                                               GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: ROberts, Chris
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47.90%
26.89%
12.80%
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Best Local Similarity:
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US-09-814-353-19577
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5720 AAAACGCACCACCAACTCGAAAA------AAACCAAATAATACACAACGTTTC 5673
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5960 TTTAAAAATCTAACCCAAAAATCTAAAAATAACGAAAAAACTTAAAATTTCT 5901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AspGlyTyrGluAsnileAspSerLeuThrArgLysValArgGlnPheArgGluArgSer 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 CysTyrThr---ValileAsnHisIleProHisGlnArgSerSerLeuSerSerAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySerGluGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GluThrGluTyrAlaLeuLeuArgThrSerValSerArgProCysSerCysThrHisGlu
                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1085
                                                                                                                                                                                                                                                                                                                                                                                             7488
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| Publication No. US20040038222A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: DIETRICH, WILLIAM
| APPLICANT: DIETRICH, WILLIAM
| TILLE OF INVENTION: ANTHRAX SUSCEPTIBILITY GENE
| FILE REFERENCE: 54991(1720)
| CURRENT APPLICATION NUMBER: US/10/261,175A
| CURRENT FILING DATE: 2002-09-30
| PRIOR APPLICATION NUMBER: 60/325,864
| PRIOR FILING DATE: 2001-09-29
| NUMBER OF SEQ ID NOS: 23
| SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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               PRIOR APPLICATION NUMBER: PCT/EPO1/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SQ ID NOS: 2424
LENGTH: 7488
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                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GluAsnGlnLysLys---
                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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US-10-261-175A-9
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DB:
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US-10-311-455-1085/c
Sequence 1085, Application US/10311455
Publication No. US20030143606A1
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Thistian
APPLICANT: DIEBENBROCK, Thistian
APPLICANT: Christian
APPLICANT: SERLIN Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REPERBROKE: 5013-1014
FULE REPERBROKE: 5013-1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAspGlnAspLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsn 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GlySerGlySerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnPheArgGluArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArg 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 4, 5, 6, 5250, 5251, 5252, 5253, 5254, 5255, 5256,
LOCATION: 1, 2, 3, 4, 5, 6, 5250, 5261
LOCATION: 5257, 5259, 5269, 5261
COTHER INFORMATION: n = A,T,C or G
US-09-814-353-19577
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Matches:
Conservative:
Mismatches:
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Gaps:
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       CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/220,661

PRIOR PILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/220,661

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 22037

SOUTHWARE: PASESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 19577
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
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47.90%
26.89%
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Query Match:
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35 CTCACATCCTTCTCCTTTGGAGAAGATGACTGTCGCTATGTCATGATCTTCAAAAG
                                                                                                                                                                                                                                                                                                                                              4 GAGAAACCACCCAGCCTCGGTGACCAGAGAGTCGGCGAGAGCCAGAGAGCAGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION MANAGEMENT APPLICATION AND MADPING OF SINGLE Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome TITLE OF INVENTION: POLYMORPHISMS in the Human Genome FILE REFERENCE: 108827.123 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT PILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-07-12 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: US 60/195,483
                                                                 FEATURE: OTHER INFORMATION: Description of Unknown Organism: KiflC nucleic OTHER INFORMATION; acid sequence
                                                                                                                                                                        651
222
511
533
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                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20020198371A1
GENERAL INFORMATION:
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                                                                                                                                                                      0.0243
90.50
36.97%
23.64%
                                  TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                    Alignment Scores:
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SEQ ID NO 9
LENGTH: 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GluGluValCysTyrThrVallleAsnHisIleProHisGlnArgSerSerLeuSerSer 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 ArgGlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 ValSerSerThrSerAsnGlnGlu------AsnGluAsnGlySerGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   812 GAGCAGCTGATGGGCTCAGATGGCAACAATTATTGGAGACCAAGGGGATTCCATTTAGA
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Sequence 10372, Application US/10027632

Sequence 10372, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-0-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 10372
LENGTH: 1173
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Best Local Similarity:
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ORGANISM: Human
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 693, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
FILE REPERBNCE: 784PCT.
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US/9/488,725
PRIOR APPLICATION NUMBER: US/9/552,317
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
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38
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Matches:
Conservative:
Mismatches:
Indels:
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                           PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10372
LENGTH: 1173
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ATE: 2000-03-29
ION NUMBER: US 60/185,218
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Human
US-10-027-632-10372
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US-10-296-115-693
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Pred. No.:
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37
20
62
31
                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 693
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-693
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90.00
38.00%
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12.59%
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Best Local Similarity:
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us-10-005-907-2.rni

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US-US-106-691B-23

Sequence 23, Application US/08306691B

Fatent No. 2744039

GENERAL INFORMATION:
APPLICANT: Calabretta, Brunc
APPLICANT: Calabretta, Brunc
APPLICANT: Calabretta, Brunc
APPLICANT: Calabretta, Brunc
APPLICANT: Chroski, Tomasz
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING CONCRESS:
ADDRESSEE: Sedied: Gender, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
COMPUTER: Pennsylvania
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: US PS/2
COMPUTER: US PS/2
COMPUTER: US PS/2
COMPUTER: US PS/2
COMPUTER: US PS/2
COMPUTER: September 15, 1994
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION: DATA:
APPLICATION: DATA:
APPLICATION NUMBER:
FILING DATE:
ANAWR: MORAC: NORTHER INFORMATION:
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                                      US-08-487-2034-5

US-09-521-976-2759

US-09-521-976-2759

US-08-786-998-8

US-08-969-987-8

US-08-977-818-3

US-08-977-818-3

US-08-977-818-3

US-08-977-818-3

US-09-146-147-3

US-09-146-147-3

US-09-022-655-997

US-09-022-655-997

US-09-023-655-997

US-09-023-655-997

US-09-023-655-997

US-09-03-120-480

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US-09-620-312D-197
US-09-540-824-23
US-09-183-861-75
US-09-022-765-75
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REGISTRATION NUMBER: 30,480
REFRENCE/DOCKET NUMBER: 8321
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
US-08-306-691B-23
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Sequence 3, Appli
Sequence 78, Appl
Sequence 30, Appl
                                                                                                                                                       April 22, 2004, 17:08:28 ; Search time 81 Seconds (without alignments) 924.918 Million cell updates/sec
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6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                              - nucleic search, using frame_plus_p2n model
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US-09-167-206-3
PCT-US93-06251-78
US-09-595-684B-30
US-09-520-312D-130
US-09-205-258-118
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US-09-566-921-32
US-08-961-527-271
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            197 AGGAACCGGAGCGCGGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCATCGACCATCGAG 256
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                                                                                                                                                                                                                                                                                         14 GluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGluMet 33
                                                                                                                                                                                                                                                                                                            34 ThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGlnGluValSerSerThr
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APPLICANT: Nandabalan, Krishnan
APPLICANT: Schulz, Vincent P.
APPLICANT: Yang, Meija
APPLICANT: Yang, Meija
TITLE OF INVENTION: NIK1 PROTEIN AND NIK1 PROTEIN COMPLEXES
FILE REFRENCE: 15966-521 NIK1 protein complexes
CURRENT APPLICATION NUMBER: US/09/167,206A
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
SOFTHARE: Patentin Ver. 2.0
LENGTH. 2301
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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US-09-167-206-3
'Sequency 3, Application US/09167206A
'Setent No. 6476193
'GENERAL INFORMATION:
TELEX: No. 5734039e
INPORMATION FOR SEQ ID No: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2301 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0132
                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
NAME/KEY: CDS
; LOCATION: (233)..(2155)
US-09-167-206-3
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                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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Pred. No.:
Score:
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Pred. No.:
                                                                                                          US-08-306-691B-23
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DB:
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PCT-US93-06251-78

PCT-US93-06251-78

Sequence 78, Application PC/TUS9306251

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TORRESPONDENCE: 93

CORRESPONDENCE: 93

CORRESPONDENCE: 93

CORRESPONDENCE: 400 Garden City Plaza

CITY: Garden City
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                                                                                                                                                                                                                        54 SerAsnGlnGluAsnGluAsnGlySerGlySerGluGluValCys------ 68
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                                                                                                                                                                                      14 GluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGluMet 33
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFEMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 19930630
CLASSIFICATION:
  24
24
34
34
Conservative:
Mismatches:
Indels:
Gaps:
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NAME: DiGiglio, Frank S.
REGISTATION UNDRER: 31,346
REFRENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELERAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 78:
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LENGTH: 2301 base pairs
LENGTH: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Zhou, Ping
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Ren, Feiyan
Chen, Rui-hong
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
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ORGANISM: Homo gapiens
FEATURE:
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US-09-620-312D-130
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Pred. No.:
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APPLICANT: Ascwicz, Roman
APPLICANT: Waisberg, Eugeni
APPLICANT: Wood, Kenneth
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TITLE OF INVENTION: and purifying human kinesins
TITLE OF INVENTION: and purifying human kinesins
TITLE OF INVENTION: WOUMBER: US/09/595,684B
CURRENT APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 30
LENGTH: 8257
                                                                                                                                                                                                                                                                                                                                            54 SerAsnGlnGluAsnGluAsnGlySerGlySerGluGluValCys----
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6544766
 DNA (genomic)
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APPLICANT: Beraud, Christophe
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90.00
49.57%
21.74%
12.59%
                                                              0.0132
96.00
41.41%
22.66%
13.43%
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Best Local Similarity:
Query Match:
                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-595-684B-30
MOLECULE TYPE:
PCT-US93-06251-78
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                                              Alignment Scores:
Pred. No.:
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3433 CTTTCTAGGACCTGTGACAGACTGAGAAGATTGAAGAAAAACTAAAGGAAAAGAGCCAG 3492
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                                                                                                                     LeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLysLysGlyAsnPro 24
                                                                                                                                                                                                                                                                                                                                                                                      25 AspGluGluArgLysArgGlnGluMetThrThrPheGluArgLysLeuGlnAspGlnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 SerGluGluValCysTyrThrVallleAsnHisIleProHisGlnArgSerSerLeuSer
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Matches:
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No. 6569662
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3433 CTTTCTAGGACCTGTGACAGACTGGCAGAAGTTGAAGAAAAACTAAAGGAAAAGAGCCAG 3492
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3553 AAAAGATTAATGAAATTTAAAGAATTTAAAGAATTAAAGAA----- 3603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 LystysSerGinGluValSerSerThrSerAsnGln---GluAsnGluAsnGlySerGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 SerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSerSerLeuSer 83
                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLysLysGlyAsnPro
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CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT PILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,896
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EARLIER APPLICATION NUMBER: 60/048,896
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,994
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,994
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,999
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,999
   Conservative:
Mismatches:
Indels:
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                                                                                                               Gaps:
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Percent Similarity:
Best Local Similarity:
Query Match:
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| MARLIER FILING DATE: 1397-06-06
| MARLIER PLING DATE: 1397-06-06
| MARLIER PRING DATE: 1397-06-06
| MARLIER PLING DATE: 1397-06-06
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682 CACAGATCAGCTGGAGCCCCGAGCAGGACAGGTGAGCCAGAGCCAGAAGCCGTTTCAAGG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 IleAspSerLeuThrArgLysValArgGlnPheArgGluArgSerGluThrGluTyrAla 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              862 AGCCCCTTCCTGCAGAAGCAACTCACTCAA.-----CCAGAAACCTCCTACGGC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 gagcgacgagagcgggagcrgcaggaggcrgccgacgrgagcagcaacaggaacag 681
                                                                                                                                                                                                                                                                                                                                                                        51 --------SerSerThrSerAsnGluAsnGluAsnGlyserGly 63
                                                                                                                                                                                                                                                                                                                                    14 GluasnGlnLysLysProLysLysGlyAsnProAspGluGluargLysArgGlnGluMet 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 --------SerSerLeuSerSerAsnAspAspGlyTyrGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-VSII-9974

US-VSII-9974

Sequence 4, Application US/08931999

Patent No. 6043219

GENERAL INFORMATION:
APPLICANT: Crupper, Scott S.
TITLE OF INVENTION:
APPLICANT: Crupper, Scott S.
TITLE OF INVENTION:
Broad Spectrum Chemotherapeutic Peptide
NUMBER OF SEQUENCES:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kanasa City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: IBR PC Compatible
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 SerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             34 ThrThrPheGluArgLysLeuGluAspGluAspLysLysSerGluGluVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910 CGAGAGCCCÁCAGCTCCTGTCTCCCGGCCTGCAGCA 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 LeuLeuArgThrSer---ValSerArgProCysSer 122
                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                     US-10-005-907-2 (1-135) x US-08-630-915A-17 (1-1302)
                                                                                                      Length:
Matches:
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APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
  DNA
                                                                                                                                                   Percent Similarity:
Best Local Similarity:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                ,
US-08-630-915A-17
                                                                                Alignment Scores:
                                                                                                                                                                                                                Query Match:
DB:
                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ThrArgLysValArgGlnPheArgGlu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 GGAGAGGAATGGGACCCCCAGAAGGCTGAGAGAAGCGGAAGCTGAAGGAGCTGGCCCAG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 ArgSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgProCysSerCysThr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511
                                                                                                                                                                                       224 ATCAAGAAAAGTTTCAGCCAATGACAAGATC-----GAGAGGAGCATACTACATGAT 277
                                                                                                                                                                                                                                                                                             278 GTGGTGGAAGTGGCTGGCCTGACATCCTTCTCCTTTGGGGAAGATGATGACTGTCGCTAT 337
                                                                                                                                                                                                                                                                                                                                                                                              338 GTCATGATCTTCAAAAGGAGTTTGCACCCTCAGATGAAGAGCTAGACTCTTACCGTCGT 397
                                                                                164 cricgagrircgiaaaaggargcagaaggaggrgrcagarircarrcaagacagrgcag 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: KOWLKES, Dana M.
APPLICANT: ROWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 AGGCAAGAGGAGGAGCCAGCCAGGAGGCCTGTGGTGGTGAGCCCTGCCAGC----
                                                                                                                                                                                                                                                                                                                                               ----GlyTyrGluAsnIleAspSerLeu-
                                                                                                                                                                                                                                           ----SerleuSerSerAsnAspAsp---
                                                                                                                                       65 GluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compartible
COMPUTER: IEB PC compartible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLLASSIFICATION: S. Leslie
RESTERRATION: S. Leslie
REFERENCE/DOCKET NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 HisGluHisAspTyrGluValValPheProHis 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  512 ------ĠAĊTAĊAAGGACAAGTACAGCĊAĊ 535
                                    ValSerSerThrSerAsnGlnGluAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Ameri CITY: New York COUNTRY: USA COUNTRY: USA ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 790-9090
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STRANDEDNESS: single
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US-08-630-915A-17
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
APPLICATION NUMBER: US/08/688,376 FILING DATE: 30-JUL-1996 CLASSIFICATION: 800
                                                ATTORNEY/AGENT INFORMATION:
NAME: Pepper, Frederick W.
REGISTRATION UNDHER: 31,268
REFERENCE/DOCKET UNDHER: 567-:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 619-464-410
TELEFRAN: 619-464-410
SEQUENCE CHARACTERISTICS:
LENGTH: 5394 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_signal
4607..4612
                                                                                                                                                                                                                                                                                                                                                                          TATA_signal 2275..2281
                                                                                                                                                                                                                                                                   linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                     NAME/KEY: C
LOCATION:
PEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY: I
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US-09-976-594-725
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US-08-688-376-1
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Sequence 1, Application US/08688376

Sequence 2, Application US/08688376

GENERAL INFORMATION:
APPLICANT: Satow, Hiroyasu
TITLE OF INVENTION: NOVEL PROCESS FOR PRODUCING SUBSTANCES
TITLE OF INVENTION: IN MAMMARY GLAND OF TRANSGENIC ANIMAL BY USING MC26 GENE
TITLE OF INVENTION: EXPRESSION-REGULATORY REGION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: DIMORTH & BARRESE
STREET: 4350 LaJolla Village Drive, Suite 300
CITY: San Diego
STREET: A. Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AspSerLeuThrArgLys------ValArgGinPheArgGlu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 ThrSerAsnGlnGluAsnGluAsnGlySerGluGluValCysTyrThrVallle 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 AsnHislleProHisGlnArgSerSerLeuSerSerAsnAspAspGlyTyrGluAsnIle 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGluMet 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 ThrThrPheGluArgLysLeuGlnAspGlnAspLysLysSerGln---GluValSerSer 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-005-907-2 (1-135) x US-08-931-999-4 (1-6755)
                                                                                                                                                                                                          ORGANISM: Staphylococcus aureus
STRAIN: UT0007
US-08-931-999-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 ArgSerGluThrGlu 109
       TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                             Alignment Scores:
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Sequence 725, Application US/09976594

Patent No. 6673549

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TILE REFREENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR APPLICATION NUMBER: 60/240,409
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 725
LENGTH: 8146
TYPE: DNA
                                                                                                                                                                1491 ------AAGAAGAAGAAGAAGAAGAAGAAGAAAAGGGAAATTAATTGGAAA 1541
                                 34 ThrThrPheGluArgiyeLeuGlnAspGlnAspiyeLyeSerGlnGluValSerSerThr 53
                                                                                                                                                                                                                          54 SerAsnGlnGluAsnGluAsnGlySerGlySerGluGluVal-----ÇysTyrThrVal 71
14 GluAsnGlnLysLysProLysLysGlyAsnProAspGluGluArgLysArgGlnGluMet 33
                                                                                                                                                                                                                                                                                                                                                                                       1602 AAGCCCTTTATTTTCCATAATCTGCACTAATGAAGGAAGA 1646
                                                                                                                                                                                                                                                                                                                                                   72 IleAsnHisIleProHisGlnArgSerSerLeuSerSerAsnAsp
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2886 GGCGAATGTGAACAGAGACCTGGAGGCCCGTCGAGAAGAGGGGGTAGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2946 ATTGAAAATTTGAAGATGAAGGAGCCGGTTTTGAAGAATCTTCAGAGACTGGAGAC--- 3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3060 CACGTATGTGTGAGGGCGCCTCCAAGCACAGCCCCACTGAGGATGAGGAAAGTGCCAAGGCG 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 TyrgluhsnileAspSerLeuThrArgLysValArgGlnPheArgGluArgSerGluThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                        26 GludiuArglysArgGlnGluMetThrThrPheGluArglysLeuGlnAspGlnAspLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlySerGlu 65
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APPLICANT: Tingley, Debora W.

APPLICANT: Edwards, Carla M.

TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REPERENCE: PA-0024 US

CURRENT APPLICATION NUMBER: US/05/566,921

CURRENT APPLICATION NUMBER: US/05/566,921

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL PROGRAM

SEQ ID NO 32

LENGTH: 11917

TYPE: NATA
                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 4295277CB1
NAME/KEY: unsure
LOCATION: 8083
CTHER INFORMATION: a, t, c, g, or other
US-09-976-594-725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

) OTHER INFORMATION: Incyte ID No. 6682888 475473.1

) NAME/KEY: unsure

; LOCATION: 3384, 10290-10321, 10325

US-09-566-921-32
                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GluValCysTyrThrVallleAsnHisIlePro-
                                                                                                                                                                                                                                                                                                                                                                13 GlyGluAsnGlnLysLysPro
                                                                                                                                                                                                                             38.02%
26.45%
11.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3234 GAG 3236
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                                                                                                                                                                        ignment Scores:
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                                                                                                                                                                                            red. No.:
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Sequence 271, Application US/08961527

Batent No. 64201305

Batent No. 64201305

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3121 GAGGCTGATGCATACATCAGGGAGAAGAGGAGTCTGTGGCCAGTGGGGATGACGAGCC 3180
                                                                                                                                                                                                                                                                                                                                                                                                                                3061 cacdrardrengadecerrecaageacaeceee 3120
                                                                                                                                                                                                 89 TyrgluasnileaspSerLeuThrargLysValargGlnPheArgGluargSerGluThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HisGlnArgSerSerLeuSerSerAsnAspAsp---Gly 88
                                                                                                                                                                                                                                              26 GlugiuargLysargGlngluMetThrThrPheGluargLysLeuGlnaspGlnAspLys
                                                                                                                                                                                                                                                                                                                       46 LysSerGlnGluValSerSerThrSerAsnGlnGluAsnGluAsnGlySerGlu
                                                                                                                                                                                                                                                                                 2947 ATTGAAAATTTGAAGATGAAGGAGCCGGTTTTGAAGAATCTTCAGAGACTGGAGAC---
                                                                                                                                                                            -- LygLysGlyAsnProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                           Conservative:
Mismatches:
Indels:
                                                                                                                                        US-10-005-907-2 (1-135) x US-09-566-921-32 (1-11917)
               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                   66 GluvalCysTyrThrvalIleAsnHisIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 271:
                                                                                                                                                                              13 GlyGluAsnGlnLysLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Andere
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                             84.00
38.02%
26.45%
11.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---------
                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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lignment Scores:
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                                                                                                                                                                                                                                                                                               19 ProlyslysgysanProAspGluGluArgLysArgGlnGluMetThrThrPheGluArg 38
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                                                                                                                                                                                                                                          321 GTCAGACCTACAGCATTGATTTGCGACTCTAİCAĞĞİİCİTA-AACTCTİĞCCAACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gGluArgSerGluThrGluTyrAlaLeuLeu----------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 ----ArgThrSerValSerArgProCysSer-----CysThrHisGlu---HisAspTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 TGABABABGABTTTCACGA---TGCAGCTACCGGTGTTCTTATCGGCCTCATCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SerGlySerGluGluValCysTyrThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 lileAsnHisIleProHisGlnArgSerSerLeuSerSerAsnAspAspGlyTyrGluAs
                                                                                                                                                                                                                                                                                                                                                                                                               -----SerThrSer-AsnGlnGluAsnGluAsnGly-----
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ADDRESSEB: Hamilton, Brook, Smith & Reymolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                              598
51
27
37
11
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APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: B.
NUMBER OF SEQUENCES: 8
                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                              JS-10-005-907-2 (1-135) x US-08-961-527-271 (1-598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/07789915A; Patent No. 5212058
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                                                                                                            0.107
82.50
41.71%
27.27%
11.54%
SEQUENCE CHARACTERISTICS:
LENGTH: 598 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                       TOPOLOGY:
US-08-961-527-271
                                                                                                 Alignment Scores:
Pred. No.:
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114
120
300
300
300
300
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,915A
FILING DATE: 19911108
CLASSIFICATION: 405
ATTORNEY/AGRAT INFORMATION:
NAME: Brook, David E.
REFERENCE/DOCKET NUMBER: MIT-5091AA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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Best Local Similarity:
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US-08-005-002C-5
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; LOCATION:
US-07-789-915A-5
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5171 ACTAAAGAAGAAGAAGAAGAAGAAGAAGGAGAACTAGATTTTATTGAAGATGACAAT 5230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: TELOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,203A
FILING DATE: US-JWN-1995
CLASSIFICATION: 435
PRIOR APPLICATION WHERE: US
FILING DATE: 15-JWN-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATENTIN, NUMBER: 35,505
REGISTRATION NUMBER: 35,505
REFERENCE/LOCKET UNMBER: MIT-5091A3Z
REFERENCE/LOCKET UNMBER: MIT-5091A3Z
                                                                                                                            Sequence 5, Application US/08487203A
Patent No. 5683904
GENERAL INFORMATION:
APPLICANT: Baler, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 207-363-0558
                                                     5453 AAAGAGGAAAATGTA 5467
                 113 LeuArgThrSerVal 117
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
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STRANDEDNESS: double
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983..4774
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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LOCATION:
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DB:
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                                                                                                                                                                                            COMPUTER EADABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/005,002C
FILING DATE: 15-JAN-1993
RIOR APPLICATION NUMBER: US 07/789,915
FILING DATE: 0-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: FATEIL, Kevin M.
REGISTRATION NUMBER: MIT-5091AAZ
FILERRANCE/DOCKET NUMBER: MIT-5091AAZ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: 207-363-0528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
TYPE: nucleic acid
STRANDBNESS: double
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: Vork Harbor
STATE: Maine
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 983
US-08-005-002C-5
                                                                                                                                                                                 03911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
INFORMATION F
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98 Lys------ValArgGlnPheArgGluArgSerGluThrGluTyrAlaLeu 112
                                                             113 LeuargThrSerVal 117
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Search completed: April 22, 2004, 18:40:34 Job time : 99 secs

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	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	ri.
OM nucleic - nuc	OM nucleic - nucleic search, using sw model	
Run on:	April 22, 2004, 11:22:40 ; Search time 3: (without align 4901.767 Mill	Search time 151 Seconds (without alignments) 4901.767 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-005-907-1_COPY_25_429 405 1 atgggaaattatctctgcgatgaagtt	.,atgaagttgtgtttccacac 405
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched:	3373863 8egs, 2124099041 residues	
Total number of	of hits satisfying chosen parameters:	6747726
Minimum DB seg	seq length: 0 seq length: 2000000000	
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	1. Geneseq 29Jan04:* 1. Geneseq1980s:* 3. geneseq1990s:* 4. geneseq12000s:* 5. geneseq12001bs:* 6. geneseq12001bs:* 7. geneseq12001bs:* 9. geneseq12003as:* 10. geneseq12003cs:* 10. geneseq12003cs:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Adc30760 Hu Abn81319 Hu Abn81319 Hu Abn81319 Hu Abs65991 Hu Abs65341 Fu Abs132700 Hu Abs132700 Hu Abs17337 Hu Abs17337 Hu Adc30201 Hu
SUMMARIES	ADC30760 ANN81319 ACC59551 ACC59551 AACC59551 AAS46328 AAS46328 AAS46328 AAS465328 AAS65119 AACC5119
DB	 0000004400000000000
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Aac77913 Human can Aat67620 H. pylori Aat68100 H. pylori Abt8921 Human che Abl32105 Human che Abl32105 Human imm Aaf4365 Retrovira Abl32783 Breast ca Abl32783 Breast ca Abl32789 UnA encod Aca4580 Prokaryot Aca50029 Prokaryot Abl3263 Human imm Ada71938 Rice gene Aaa70236 Plasmodlu Adc8768 Human amm Abl38491 Human col Abg34463 Oligonucl Abg51819 Oligonucl Abg51819 Oligonucl Abg51819 Oligonucl Abg51819 Oligonucl	· ·	NO:842. forensics; gene mapping; s disease; Alzheimer's disease; s platelet disorder; wound; burns; lease; cancer; lement; antiparkinsonian; nootropic; coagulant; thrombolytic; vulnerary; ressive; antiinflammatory; cytostatic; ss.	Zhao QA, Wang J, Wehrman T; Asundi V, Wang Z, Weng G;	useful for diagnosing, preventing or generative diseases, anemias, platelet steoporosis, autoimmune diseases or lish.
AAC77913 AAT67620 AAT68100 ABK33921 ABK332105 AAF24365 ABH32749 ABH32749 ABH3263 ABH3263 ABH3268 AAA70236 ABH3369 ABH33463 ABQ31463 ABQ31463 ABQ31463	ALIGNMENTS	diagnostic; drug screening; for arsity assessment; Parkinson's descentative diseases; anaemia; prosteoporosis; autoimmune diseases; anaemia; prosteoporosis; autoimmune diseases; autoimmune diseases; autoimmune diseases; autoimmune diseases; autoimmune diseases; autoimmune diseases autointo autoimmune diseases autointicos autoimmune diseases; osteopathic; immunosuppresseres; obtomosome 1; gene; ss. apiens.	Xue AJ, Ma Y,	eptide u neurodeg cers, os pp; Engl novel h
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4 R 0 7 C 8 Q 0 1 L 2 E 4 R 0 7 C 8 Q 0 1 L 2 E 4 R 0 9 C 1 L 2 E 4 R 0 9 C 1 L 2 E 4 R 0 9 C 1 L 2 E 4 R 0 9 C 1 L 2 E 4 R 0 8 C 1 L 2 C 1 L 2 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C	1 50 5030760 st 5030760; 3-DEC-2003	Human novel cDNA s Human; diagnostic; biodiversity asses neurodegenerative ulcers; osteoporos molecular weight m neuroprotective; antiulcer; osteopa gene therapy; chro Homo sapiens. WOZO03029271-A2.	4-SEP-200 4-SEP-200 HYSE-) HY ang TY, hou P, G aley-Vice PI; 2003-	New polynucleotide treating conditions disorders, wounds, lcancer. Claim 1; SEQ ID NO The invention relat
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30-AUG-2002 (first entry)

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control also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody complete of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliocathing a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention carrier and/or monoclonal antibodies for the cDNA sequences of the invention of contig sequences corresponding to the cDNA sequences of the invention are expression or activity, and the polypeptides encoded by the contigs (ADC33262) and the polypeptides encoded by the contigs (ADC3334). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, burns, diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases. Alzheimer's conner. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, cand as food supplements. The present sequence represents a specifically of the patent did not form part of the printed specification, but was contained in electronic format directly from WIPO at the patent did not form part of the printed sequence of the printed in electronic for
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Best Local Similarity 100.0%; Pred. No. 2.9e-107;
Matches 405; Conservative 0; Mismatches 0; Indels (
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ABN81319 standard; cDNA; 3762 BP.

ABN81319

RESULT 2
ABN81319
ID ABN8
XX
AC ABN8

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The invention relates to isolated mucleic acid (ABN81319-ABN81324),

corresponding to genes differentially expressed in mast cells following

activation or in pairents with allergic hypersensitivity disease, (I)

that encodes proteins (ABB77559-ABN87575) (II) or a protein fragment of

(II) if at least 6 amino acids. (II) is useful for identifying binding

partners. (I) or (II) is useful for diagnosing or treating a disease

partners. (I) or (II) is useful for diagnosing or treating binding

partners. (I) or (II) is useful for diagnosing or treating binding

cuticaria or atopic dermatitis or mastocytosis) in a subject which

involves determining the level of expression of (I) or (II). A computer

system, comprising a database containing information identifying the

expression level in a tissue or at least one mast cell of (I), is useful

for presenting information to identify the relative expression level of

(II) is used as a marker to detect, diagnose or identifying

response in a patient. The protein can also serve as a target that

modulate gene expression of activity and as an antigen to raise

collistic or antagonists. The agonists or antagonists are useful for

modulating biological activity and function of (II) and thus are useful

condulating disease conditions such as allergic hypersensitivity,

seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis
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                                                                         Human, mast cell; MC, antiallergic; antiinflammatory, antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAG
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Pred. No. 5.4e-107;
                                  Human mast cell related gene MC1 SEQ ID NO 1.
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25. .432
/*tag= a
/product= "MC1"
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                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2000; 2000US-0251835P.
14-MAR-2001; 2001US-0275479P.
28-MAR-2001; 2001US-0279115P.
02-AFR-2001; 2001US-0280143P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                        WO200246389-A2.
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                                                                                                                                                       Homo sapiens.
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                                                                                                                gene; ss.
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204
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                                                                                                                                                                                           Human, immune response associated protein; IRAP; anti-HIV; antiallergic; antinflammatory; antianaemic; antiparkinsonian; noctropic; antithyroid; anticortusant; antiartersioscleroits; antiasthmatic; immunosuppressive; cytostatic; hepatotropic; dermatological; antidabetic; nephrotropic; antigotal; antidabetic; nephrotropic; antiparasitic; antibariantic; antibariantic; antiparasitic; antibariantic; antiparasitic; antibariantic; uropathic; protozoacide; antirheumatic; haemostatic; antibacterial; virucide; ophthalmological; fungicide; gene therapy; immune system disorder; neurological disorder; developmental disorder; muscle disorder; cell proliferative disorder;
                                                                                        205 GGCAGTGGTTCTGAAGAAGTGTGCTACAGTCTCATTAATCACATCCCCCATCAGAGATCC
                                                                                                                                           145 CAAGATCAAGATDAAGAAAAGCCAAGAAGTTTCATCACTTCTAATCAGGAAAACGAGAAAT
                                                                          181 GGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCC
                                                                                                                                                                             CAGITIAGAGAAAGGICAGACAGAAIAIGCCCTICIIAGGACIICTGIIAGIAGGCCI
                        CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT
                                                                                                                                                                                                                                            TGTTCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCCACAC 405
                                                                                                                                                                                                                                                                                                                                                                                               Human IRAP-28 encoding cDNA SEQ ID NO:63
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134. .670
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2001US-0328923P.
2001US-0344468P.
2001US-034240P.
2001US-03420282P.
2002US-0347693P.
2002US-0358279P.
2002US-036494P.
                                                                                                                                                                                                                                                                                                                      ACC59951 standard; cDNA; 732
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12-OCT-2001;
19-OCT-2001;
09-NOV-2001;
21-NOV-2001;
07-DEC-2001;
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20-FEB-2002;
01-MAR-2002;
15-MAR-2002;
10-MAY-2002;
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2002US-0379876P 2002US-0388180P

(INCY-) INCYTE GENOMICS

11-JUN-2002;

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ACC59924 to ACC5958 encode the human immune response associated proteins of given in ABR4205 to ABR42239, designated IRAP-1 to IRAP-29 (1). (1) have given in ABR4205 to ABR42239, designated IRAP-1 to IRAP-29 (1). (1) have contributed anticallergic, anticallergic, anticallergic, anticallergic, anticallergic, anticallergic, antichronoid, cytostatic, hepatotropic, dermatological, antichronoid, cytostatic, hepatotropic, dermatological, antichronoid, cytostatic, natibacterial, uropathic, ophthalmological, antichromimetic, antibacterial, uropathic, ophthalmological, antichromatic, hemostatic, antibacterial, virucide, ophthalmological, antichromatic, antibacterial, virucide, ophthalmological, antichromatic, and antagonists are useful for Human IRAP polymucleotides, agonists and antagonists are useful for chargesing or preventing disorders associated with aberrant allergies, autoimmune thyroiditis, contact dermaticis, Crohn's disease, allergies, autoimmune thyroiditis, contact dermaticis, Crohn's disease, disease, Hashimaco's thyroiditis, irritable bowel syndrome, gout, cromaticis, coteoprosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sigoren's syndrome, uveitis), cycloporosis, pancreatitis, anaemia cor mental retardation, muscle disorders (e.g. cardiomyopathy, myocarditis or mental retardation), muscle disorder (e.g. cardiomyopathy, myocarditis, cor nermaclyositis), call proliferative disorders (e.g. arteriosclerosis, carchols, paroxysmal nocturnal harman paramia, polycythemenia vera, psoriasis, primary thrombosytopaemia or cancer), or viral, bacterial, fungal, parasitic, representation, or varial, paroxysmal nocturnal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
                                                                                                                                                                                                                                      New human immune response associated proteins and polynucleotides, useful for diagnosing, treating or preventing immune system disorders, e.g. AIDS or anemia, cell proliferative disorders, e.g. cancer, or neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 TGTTAGTAGGCCTTGTTCCTGCACCCATGAGCATGATTATGAAGTTGTGTTTCCACAC 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 CGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AAAGAGGCAAGATTCCCAAAACGAAAATGAAAGAATGTCATCTACTCCCATCCAGGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
Ho A, Baughn MR, Becha SD, Burford N, Elliott VS, Emerling BM; Forsythe IJ, Gorvad AE, Griffin JA, Hafalia AJA, Honchell CD; Ison CH, Burrill JD, Blake JJ, Lal PG, Lee EA, Marquis JP; Lehr-Mason PM, Lee S, Sprague WW, Swarnakar A, Tang YT, Tran B; Tran UK, Bhatia U, Chawla NK, Warren BA, Zheng W, Xu Y, Yue H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.4%; Pred. No. 1.3e-06;
Matches 162; Conservative 0; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 208; 213pp; English.
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                                                                                                                                                                  WPI; 2003-363161/34.
                                                                                                                                                                                            P-PSDB; ABR43232
                                                                                                                                                                                                                                                                                                                                disorders.
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Polynucleotide sequences encoding human secretory proteins useful for gene therapy of e.g. genetic deficiency disorders, cancers, and diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 275-276; 585pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy of e.g. genetic defic
caused by intracellular parasites.
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                                                                                                                 WO200220756-A2.
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06-SEP-2000;
06-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
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                                                                                                     Homo sapiens
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2002-315658/35.

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of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and protozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell paralites (e.g. fungal mamune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's disease), motor neuron disorders, demyelinating diseases (e.g. Parkinson's disease), motor neuron disorders, prion diseases, cerebral palsy, neuroskeletal disorders, peripheral nervous system disorders, unltiple sclerosis), meningitis, abscesses, prion diseases, cerebral palsy, neuroskeletal disorders, peripheral nervous system disorders, and mental disorders (e.g. Tourette's syndrome). CDNA sequences ABL99746 - ABL99929 represent human secretory polynualectides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1643 BP; 413 A; 382 C; 384 G; 460 T; 0 U; 4 Other;
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                                                                                                                                                                         Human; s8; gene; secretory protein; secretory polynucleotides; SPTM; SPTM-related disease; somatic gene therapy; germline gene therapy; severe combined immunodeficiency; intracellular parasite protection; fungal parasite; protozoan parasite; cell proliferative disorder; cancer; motor neuron disorder; AIDS; neurological disorder; Parkinson's disease; meningitis; abscess; prion disease; multiple sclerosis; neuroskeletal disorder; peripheral nervous system disorder; dermatomyoskiis; polymyositis; myopathy; myasthenia gravis; mental disorder; Tourette's syndrome.
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                                                                                                                                Human secretory polymucleotide (sptm) 46.
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2000US-0229748P.
2000US-0229751P.
2000US-0230016P.
2000US-023051P.
2000US-023051P.
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2000US-023059P.
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07-SEP-2000; 2000US-0230896P.
07-SEP-2000; 2000US-0230897P.
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07-SEP-2000; 2000US-0231832P.
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                                                                            03-OCT-2002 (first entry)
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1236 ATGGAAAAAAATACTCATTTTTGAAAAGAGGCAAGATTCCCAAAAGGAAAGAATGAAAGAAT 1295
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                                                                                                                                                                                                                                                                                                                                                               87 ACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGA 146
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Query Match
11.7%; Score 47.2; DB 6; Length 1643;
Best Local Similarity 50.8%; Pred. No. 0.0024;
Matches 165; Conservative 0; Mismatches 154; Indels 6
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The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics, encode. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, medical imaging, identification of mutations and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or amino acid sequences. They are also useful for preventing, treating or amino acid sequences. They are also useful for preventing, treating or amino acid sequences. They are also useful for preventing, treating or amino acid sequences, neurodegenerative disorders, osteoporosis, osteoarthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, acopic dermatitis). Sequences ABX04986-ABX05511 represent human polymucleotides of the cinvention. Note: The sequence data for this patent is not represented in the Brinted specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                               treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative disorders, and infections.
                                                                                                                                                                                                              New isolated polypeptides and polynucleotides, useful for preventing,
                                      Goodrich R, Asundi V, Zhang J, Zhao QA, Re
Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
J, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 123; 235pp; English.
                                                                    Xue AJ, Yang Y, Ma
Wehrman T, Wang J,
                      Zhou P,
                                                                                                                                           WPI; 2003-040556/03
                                                                                                                                                                     P-PSDB; ABU00030,
                                                               ·Yang
                                                rang YT,
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11.5%; Score 46.6; DB 7; Length 775; llarity 50.8%; Pred. No. 0.0027; Conservative 0; Mismatches 154; Indels Sequence 775 BP; 226 A; 202 C; 160 G; 187 T; 0 U; 0 Other; Query Match

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564
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                                                          87 ACGCCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGA 146
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Best Local Similarity
Matches 165; Conserv
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Tumour suppressor gene derived chemically modified sequence #50.

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with being blailphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and complementary to (58). The nucleic acid may be a peptide nucleic acid complementary to (58). The nucleic acid may be a peptide nucleic acid coligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleic playmorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or active probes can also be used in a method for ascertaining genetic and/or copression to pacific diseases, by analysing diseases or the predisposition to specific diseases, by analysing cycosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters in the disposis events which are disadvantageous to parients. The present sequence is one of the 533 genomics sequence is one of the 533 genomics sequence of the corresponding odd numbered sequence is one of the 233 genomics sequence of the corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and ID. Corresponding odd numbered sequence (e.g. ID 2 and IDI. ID 536 and IDI. Corresponding observable and proper partner sequence is missing). Note: The set of the printed pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%; Score 41.6; DB 4; Length 6446; 56.6%; Pred. No. 0.16;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 50; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K;
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                                                                                                                                                                                                                                                                                            15-WAR-2000; 2000DE-01013847.
06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01043826.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                       15-MAR-2001; 2001WO-EP002955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-602752/68.
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                                                                                                                                                      WO200168912-A2
                                                                                                         Homo sapiens
                                                                                                                                                                                                        20-SEP-2001
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99 GACTACATITGAAAGAAAACTICAAGAICAAGATAAGAAAAAGCCAAGAAGTITCATCCAC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
                                                                                                                                              Tumour suppressor gene derived chemically modified sequence #63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18988 BP; 4826 A; 567 C; 4681 G; 8914 T; 0 U; 0 Other;
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10.3%; Score 41.6; DB 4; Length 189
Best Local Similarity 47.3%; Pred. No. 0.24;
Matches 125; Conservative 0; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 63; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                       BD.
                                       AAS46341 standard; DNA; 18988
                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UUN-2000; 2000DE-01052529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2001; 2001WO-EP002955.
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                   WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2000;
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                             18-DEC-2001
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RESULT 7
AAS46341/c
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18167
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                                         218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic, antianaemic; cytostatic, nootropic;
neuroprotective, anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsortatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Albrieme; a disease; AlDS; epileps;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                          18226 icraaaicaaraaacriraccaacrafarcaarrirarcaccacraficaa
                                                                                                                 219 TCACATCCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGATGATGAGCTATGAGAACATTGA
                                       159 ITCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGTGCTACACTGATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.3%; Pred. No. 0.24;
Matches 125; Conservative 0; Mismatches 139; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 673; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 673.
                                                                                                                                                                                                                                   279 CTCCCTCACAAGGAAAGTGAGACA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                                       ABL32700 standard; DNA; 18988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylation.
                                                                                                                                                                                                                                                                                                                                                                            ABL32700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            olek A,
                                                                                                                                                                                                                                                                                               RESULT 8
ABL32700/c
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                                                    158
                                                                                                                                                                                                                                         TICIAAICAGGAAAACGAGAAIGGCAGIGGIICIGAAGAAGIGIGCIACACIGICATIAA 218
                                                                                                                                                                                                                                                                                                                                                                  278
98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid derived from chemically treated metastasis genes, usediagnosis of cancers by analysis of cytosine methylation, also for
                                                                                                                  99 GACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCAC
                                                                                                                                                                                                                                                                                                                                                                     TCACATCCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGGCTATGAGAACATTGA
   Sequence 18988 BP; 4826 A; 567 C; 4681 G; 8914 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
10.3%; Score 41.6; DB 6; Length 18988;
Best Local Similarity 47.3%; Pred. No. 0.24;
Matches 125; Conservative 0; Mismatches 139; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metastasis associated gene; cytostatic; gene therapy; cancer; cytosine methylation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 61; 23pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human metastasis associated gene SEQ ID NO: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18106 АССССТССАТААААААТААСАСА 18083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 CTCCCTCACAAGGAAAGTGAGACA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
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30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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39 AGAGAATCAAAAGGAAGCCCAAGAAAGGAAACCCAGATGAGGAAAAGAAAAGGCGCAGGAAAT

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonuclectides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genemic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                              18226 rcraaarcaaaacaaacriraccaacrararcaararrarrarcaccacracrarcaa 18167
                                                                                                                                                                                                                                               18166 CAÁCCAATTATTCACAAAÁTATCTCCTATTCAÁÁACATCGAACAACAACATTATCÁCCCTAÁ 18107
18346 AAAATATTAAAATAATTATGAAATATAATACTTATCAACAACATAAACCCCAAAAAAA 18287
                                                                               18227
                                                                                                                                                                                                        278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
                                                                          219 TCACATCCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGATGGCTATGAGAACATTGA
                                         99 GACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCAC
                                                                                                                         159 ITCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3equence 18988 BP; 4826 A; 567 C; 4681 G; 8914 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 1; SEQ ID NO 93; 24pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemically treated cell signalling DNA sequence#47.
                                                                                                                                                                                                                                                                                                                               18106 ACCCCCCCATAAAAAATAACACA 18083
                                                                                                                                                                                                                                                                                         279 CICCCICACAAGGAAAGIGAGACA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin K;
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ABL70203/c
ID ABL70203 standard; DNA; 18988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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tumour; cytostatic; ds
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Gaps

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Indels

Length 18988;

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8286 AACAÁTTTACAÁAAAAAAAACCAÁÁATTCAÁCAACCTÁÁTATCAÁACÁACAÍTTTTCCTC 18227
                                                                                                                                                                                                             18166 CAACCAATTATTCACAAAATATCTCCTATCAAAACATCGAACAACCTATCACCCTAA 18107
                                                                                      Human, brain expressed exon, gene expression analysis; probe, microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhaimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                           GACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAAGCCAAGAAGTTTCATCCAC
                                                                                                                                                                                                                                          219 TCACATCCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGACTATGAGAACATTGA
                                                                                                                                                                              TTCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGAGTGTGCTACACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 17828; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe SEQ ID NO: 17828.
 Score 41.6; DB 6; Pred. No. 0.24; 0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                18106 accccrccaraaaaaaaacaca 18083
                                                                                                                                                                                                                                                                                                       279 CTCCCTCACAAGGAAAGTGAGACA 302
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30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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AAK17837 standard; DNA; 1145
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10.3%;
ilarity 47.3%;
Conservative
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           al Similarity
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                                                                                                                                                                                               241
                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                             121
                                                                                                                                               181
                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                               122 AAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATG
                                                                                                                       877 ATGABAAGTCAGAAAAGAAACACAACACCCATGAAGTTTCTCCTGAACAGCCTAAAGACC
                                                                                                                                                                                               GCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCT
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                               CCCTGAGCTCCAATGATGATGACTATGAGAACATTGACTCCCTCACAAGGAAA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 5110; 650pp + Sequence Listing; English
                                                4; Length 1145;
                      0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID NO: 5110
                                                                     Mismatches 120;
                      ë
                                                         0.13;
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                      Sequence 1145 BP; 232 A; 264 C; 203 G; 446
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                                                Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00698408.
03-MJG-2000; 2000US-00632366.
31-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                       AAK05119 standard; DNA; 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312P.
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2000GB-00024263
                                                10.1%;
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                                                                      Conservative
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                                                            Similarity
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                                                                        Matches 113;
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ID AAK0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                   241
                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 971 movel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31880). The invention also relates to nucleic acid sequences over 99% identical with the movel human cDNAs. The invention additionally encompasses expression
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; diagnostic; drug screening; forensics; gene mapping; blodiversity assessment; Parkinson's diaease; Althaimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; mond, burns; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                          1187 ATGAAAAGTCAGAAAAGAAAACACAAACCCCATGAAGTTTCTCTGAACAGCCTAAAGACC
                                                                                                                                    122 AAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATG
                                                                                                                                                                                   182 GCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCT
                                                                                                                                                                                                           1067 AAGAGAGTCAAGAAGGAAAGGAAAGACACTTTTAAAAAAGATAGCCAACAAGATATTCCTT
                                                           Gaps
                                                                                                                                                                                                                                    242 CCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAA 294
                                                                                                                                                                                                                                                            1007 CCAGCAAGGACCATAAAGAGAAGTCTGAGTTTGTTGATGACATAACTACTAGA 955
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                                 Score 41; DB 4; Length 1996;
Pred. No. 0.16;
0; Mismatches 120; Indels
           Sequence 1996 BP; 487 A; 410 C; 341 G; 758 T; 0 U; 0 Other;
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ', Ren F, Xue AJ, Zhao QA,
Wang D, Ma Y, Asundi V,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                Human novel cDNA sequence, SEQ ID NO:283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 283; 1185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; chromosome 3; gene; ss.
                                                                                                                                                                                                                                                                                                                        ADC30201 standard; cDNA; 11924 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-2001; 2001US-0324631P.
                                  Query Match
Best Local Similarity 48.5%;
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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P-PSDB; ADC31172.
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Ghosh M,
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Zhou P, (
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recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The identifying a compound which binds to a polypeptide of the invention. The identifying a medical condition; kits comprising polymotecride probes and/or monoclonal antibodies for carrying out the methods of the expression or activity of the polymotecride and/or polypeptide of the invention arctivity of the polymotecride and/or polypeptide; and 767 contig sequences corresponding to the compounds that modulate the expression or activity of the polymotecride and/or polypeptide; and 767 contig sequences corresponding to the contegs (ADC3262) and the polymotecride and/or polypeptides of the invention are useful in diagnostics, drug screening, forensics gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are classification diseases such as Parkinson's diseases and other treating diseases such as Parkinson's diseases or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation probes or cancer. The nucleic acids may also be used as hybridisation as specifically, and as food supplements. The presents sequence represents a specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the print from FIPO at the printed specification.
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vectors and host cells comprising a nucleic acid of the invention;
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les 113; Conservative
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1168 AAGAGAGTCAAGAAAGAAAGGAAAGACACTTTTAAAAAAGATAGCCAACAAGATATTCCTT 1227

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WO2003029271-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Wang D, Ma Y, Asundi V, Wang Z, Weng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to 971 novel human cDNA sequences (ADC29919-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11951 BP; 3967 A; 2711 C; 2434 G; 2839 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 282; 1185pp; English.
                                                  24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                          Haley-Vicente D, Drmanac RT;
                                                                                              24-SEP-2001; 2001US-0324631P.
                                                                                                                                                                                                                                                                                          WPI; 2003-371981/35.
P-PSDB; ADC31171.
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Ghosh M,
                                                                                                                                                 (HYSE-) HYSEQ INC.
  10-APR-2003
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Zhou P,
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Zhong M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
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Ellerman K, Berghs C, Rothenberg ME, Guo X
Catterton E, Kekuda R, Ji W, Miller CE;
Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
                                            242 CCCTGAGCTCCAATGATGATGACTATGAGAACATTGACTCCCTCACAAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                      Human; NOV; gene therapy; endocrine related disease; diabetes;
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                                                                                                                                                                                                                                                                                                                                     cDNA encoding novel human protein #120.
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                                                                                                                                                                                ACD19440 standard; cDNA; 14994 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0322636P.
2001US-032281EP.
2001US-0322817P.
2001US-0323519P.
2001US-0323519P.
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2001US-0318430P.
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2001US-0325091P.
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2002US-00236177
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Leach MD,
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cc associated with a human disease, which includes a pathology associated consisted with a human disease, which includes a pathology associated the with NOVX polypeptide. The DNA encoding the protein is useful in generatherapy for treating the disease or condition. In particular, the NOVX cc polypeptide or polynuclectide is useful for treating endocrine/ cc metabolism-related diseases (e.g. obseity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, cc and inflammatory disease, rhewmaton's disease, useful arthritis or asthmatory bowel disease, rhewmatorid arthritis or stecarthritis), cancers, or melanoma), liver disease, ovarian, co prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic capplications, and for monitoring the effects of drugs during clinical trials. This sequence encodes a novel human NOV protein

XX Sequence 14994 BP, 4902 A, 3673 C, 3081 G, 3338 T, 0 U, 0 Other,
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1220 AAGAGAAACTCAGAGTTTATCTGAAACCTTGGAAATTACTATTTCAGAAGGAGGAGATCA 4279 4280 AAGAGAGTCAAGAAGAAAGGAAAGGACACTTTTAAAAAAGATAGCCAACAACATATTCCTT 4339 241 122 AAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATG 181 182 GCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCGCCCATCAGAGATCCT 0; Gaps 242 CCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAA 294 DB 7; Length 14994; Score 41; DB 7; Length 149 Pred. No. 0.33; 0; Mismatches 120; Indels Query Match
Best Local Similarity 48.5%;
Matches 113; Conservative g 셤 8 유 ઠે ò

Search completed: April 22, 2004, 14:55:21 Job time : 359 secs

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April 22, 2004, 15:25:28; Search time 336 Seconds (without alignments) 5434.506 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0, Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
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		Description	Seguence 1, Appli	Sequence 50, Appl	Sequence 63, Appl	Sequence 673, App.	Sequence 61, Appl	Seguence 27195, A	Sequence 10574, A	Sequence 96139, A	Sequence 223, App	Sequence 307, App	Sequence 913, App	Sequence, 4490, Ap	Sequence 4492, Ap	Sequence 4491, Ap
Sorres		dit.	US-10-005-907-1	US-10-221-714A-50	US-10-221-714A-63	US-10-311-455-673	US-10-240-485-61	US-09-864-761-27195	US-09-864-761-10574	US-10-424-599-96139	US-09-925-301-223	US-09-925-301-307	US-10-087-192-913	US-10-335-977-4490	US-10-335-977-4492	US-10-335-977-4491
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d	Query	Match	100.0	10.3	10.3	10.3	10.3	10.1	10.1	10.0	9.0	8.6	9.6	7.6	7.6	7.6
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	Sequence 157798, Sequence 722, App Sequence 3047, A Sequence 37450, A Sequence 37899, A	Sequence 636, App Sequence 1, Appli Sequence 2, Appli Sequence 95566, Ap Sequence 2080, Ap		Sequence 171934, A Sequence 250669, Sequence 250669, Sequence 1610, Ap Sequence 17092, App Sequence 2228, Ap Sequence 2228, Ap Sequence 9958, Ap Sequence 9958, Ap
5 US-10-311-455-78 7 US-10-257-166-2 6 US-10-125-968-1156 3 US-10-424-599-101964 3 US-10-027-632-157798	6 US-10-027-632-157798 5 US-10-311-455-722 3 US-10-244-599-30047 3 US-10-282-122A-37450 3 US-10-282-122A-37899	9555	5 US-10-146-502-2080 5 US-10-146-502-2080 5 US-10-11-455-1385 1 US-10-311-455-1985 5 US-10-311-455-1931 3 US-10-424-599-18709	13 US-09-11/883 13 US-110-424-599-11/883 13 US-110-027-632-250669 15 US-110-311-455-1610 15 US-110-311-455-1610 10 US-09-764-891-7092 13 US-09-938-842A-2228 14 US-09-918-995-9958
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ALIGNMENTS

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Sequence 1, Application US/10005907
Publication No. US20030166881A1
APPLICANT: Union Chimique Belge, S.A.
APPLICANT: Union Chimique Belge, S.A.
APPLICANT: No. US20030166881Aka, Karl
APPLICANT: No. US20030166881Aka, Karl
APPLICANT: Einerein, Richard
TITLE OF INVENTION: ACTIVATION
FILE REPERENCE: 053529-5005
CURRENT APPLICATION NUMBER: US/10/005,907
CURRENT PILING DATE: 2011-12-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAMES/KEY: CDS
; LOCATION: (25)..(432)
; OTHER INFORMATION:
US-10-005-907-1
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                                                                       145 CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAAT 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WESULT:

US-10-221-714A-50/C

Sequence 50, Application US/10221714A

Sequence 50, Application US/10221714A

PUBLICATION NO. USCO040048254A1

GENERAL INFORMATION:

APPLICANT: OLEX, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TILLE OF INVENTION: Unmor suppressor genes and oncogenes

TILLE OF INVENTION: Unmor suppressor genes and oncogenes

FILE REFERENCE: 5013.105

CURRENT APPLICATION NUMBER: US/10/221,714A

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: DE 10019058 8

PRIOR PILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

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Sequence 673, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: DIEX, Alexander
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BIEFLY, Kurt
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: 1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
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) ORGANISM:
PERTURE:
PERTURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-63
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GENERAL INFORMATION:
APPLICANT: OILEK, Alexander
APPLICANT: DIEENBROCK, Christian
APPLICANT: BIEBNBROCK, Christian
APPLICANT: BIEBNBROCK, Christian
APPLICANT: BERENBROCK, Christian
TITLE OF INVENTION: tumor suppressor genes and oncogenes
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: PCT/EP01/02955
FRIOR APPLICATION NUMBER: PCT/EP01/02955
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: DE 10019658.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
SEQ ID NOS: 540
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Best Local Similarity 47.3%; Pred. No. 0.52;
Matches 125; Conservative 0; Mismatches 139;
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-61
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APPLICANT: OLEK, ALEXANDER

APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt

ITILE OF INVENTION: Diagnosis of Diseases Associated with
ITILE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT PILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
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PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
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10.3%; Score 41.6; DB 15;
Best Local Similarity 47.3%; Pred. No. 0.52;
Matches 125; Conservative 0; Mismatches 139;
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Pred. No. 0.52;
               PRIOR APPLICATION NUMBER: L. PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 673
LENGTH: 18988
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Publication No. US20030148327A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FILING DATE: 2001-07-02
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Best Local Similarity
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPRENCES: Acond.ca.X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-0e-22
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                                                                                                                                                                                                                                                                                 219 TCACATCCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGATGATGACATTGA
                                      99 GACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCAC
  Gaps
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Indels
Mismatches 139;
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ION NUMBER: PCT/US01/00668
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PRIOR FILING DATE: 2000-02-04
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Patent No. US20020048763A1
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  Conservative
Matches 125;
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APPLICANT: LA Rosa Thomas J
APPLICANT: LA Rosa Thomas J
APPLICANT: LA Rosa Thomas J
APPLICANT: Kovalide David K
APPLICANT: Zhou Yihna
APPLICANT: Zhou Yihna
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT EXPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 10554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: MAP TO AC004886.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
US-09-864-761-10574
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10.0%; Score 40.4; DB 13;
Best Local Similarity 54.8%; Pred. No. 0.3;
Matches 80; Conservative 0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_57824C.1
US-10-424-599-96139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 96139, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-10-424-599-96139
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LENGTH: 1015
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US-09-864-761-10574/C

US-09-864-761-10574/C

Sequence 10574, Application US/09864761

Parent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chan, Weneheng GRNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION HUMBER. US/09/864,761

TITLE OF INVENTION HUMBER: US 60/180,312

PRIOR PELICANTION NUMBER: US 60/180,312

PRIOR APPLICANTION NUMBER: US 60/207,456

PRIOR APPLICANTION NUMBER: US 60/207,456

PRIOR APPLICANTION NUMBER: US 60/207,456

PRIOR APPLICANTION NUMBER: US 60/207,666

PRIOR APPLICANTION NUMBER: US 60/207,666

PRIOR APPLICANTION NUMBER: PCT/US01/00666

PRIOR PRILING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-10-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

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PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     877 ATGAAAAGTCAGAAAAGAAACACACACCCCATGAAGTTTCTCCTGAACGCCTAAAGACC 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   817 AAGAGAAAACTCAGAGTTTATCTGAAACCTTGGAAATTACTATTTCAGAAGAGAGATCA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 GCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  757 AAGAGAGTCAAGAAGAAAGGAAAGGCACTTTTAAAAAAGATAGCCAACAAGATATTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 CCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697 ccagcaaggaccaraaagagagrcrcagrrrcrrcargargacaraacracraga 645
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                                                                                                                                                                                                                                                      CTHER INFORMATION: MAP TO AC004886.1

CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EST HUMAN HIT: AIG36014.1, EVALUE 0.00e+00

CTHER INFORMATION: SWISSPROT HIT: P38254, EVALUE 7.50e-01

OTHER INFORMATION: NT HIT: AF138789.2, EVALUE 0.00e+00

US-09-864-761-27195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.1%; Score 41; DB 9; Length 1145; ilarity 48.5%; Pred. No. 0.21; Conservative 0; Mismatches 120; Indels
                                              Annomax Sequence Listing Engine vers. 1.1
       NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence 3
SEQ ID NO 27195
LENGTH: 1145
                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 113; Conserv
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PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFWARE: Patentin Ver. 2.0
LENGTH: 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-335-977-4490
; Sequence 4490, Application US/10335977
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.4%;
Matches 80; Conservative (
                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-301-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-087-192-913/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                     Sequence 223, Application US/09925301

Sequence 223, Application US/09925301

Batent No. US2020052308A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: PA106

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR PLING DATE: 2001-03-08

PRIOR PLING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE PATENTION NUMBER: 6/124,270

PRIOR FILING DATE: 1999-03-12

SOFTWARE PATENTION NUMBER: 20,124,270

FRIOR PILING DATE: 1999-03-12

LENGTH: 2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.9%; Score 40; DB 9; Length 2921; Best Local Similarity 54.1%; Pred. No. 0.63; Matches 79; Conservative 1; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 307, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO6
CURRENT APPLICATION NUVBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2862 AAAAAAAAAAAAAAAAAAAAAAAA 2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: (1609)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (2919)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (2920)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (2921)
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                                                                                                                              122 AAGATCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                    855 адаладаладаладаладаладала 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-925-301-307
                                                                                                                                                                                                                                                   US-09-925-301-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                     40 GAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGATGAGGAAAAGAAAAACGGCAGGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 39.8; DB 13; Length 56258; Best Local Similarity 60.7%; Pred. No. 2.8; Matches 65; Conservative 0; Mismatches 42; Indels 0;
                                                     ;
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DB 9; Length 785;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brockerion of APPLICANT: Brockerion of APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OANGER FILE REFERENCE: 529452000122
CURRENT PRILIAG DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-13-02
PRIOR PLING DATE: 2000-13-02
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-02
SOFURMER OF SEQ ID NOS: 2059
SOFURMER PASSER FOR WINDOWS VERSION 4.0
SEQ ID NO 913
LENGTH: 56258
                                                     67;
Score 39.8; DB
Pred. No. 0.39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                         121 CAAGATCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                                                                                                                                                                                                                         749 AAAAAAAAAAAAAAAAAAAAAAAAAA 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 913, Application US/10087192 Publication No. US20020182586A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(56258)
OTHER INFORMATION: n = A,T,C or G
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ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
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US-10-335-977-4491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLCOBACTER PYLORI
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.7%; Score 39.2; DB 13; Length 489; Best Local Similarity 64.1%; Pred. No. 0.47; Matches 59; Conservative 0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 ACTTCAAGATCAAGATAAGAAAGCCAAGAAG 148
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                                                                                                                                                                                                                                                                     CITY: Boston
CITY: Boston
COMPURY: USA
COMPURY: USA
ZIF: 02109-1875
COMPURY: USA
COMPURY: ISB PC Compatible
OPERATING SYSTEM: Mindows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILLING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILLING DATE: 17-DEC-197
ATTORNEY/AGENT INFORMATION:
NAME: Mandragourae, Amy E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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; LOCATION: (B) LŌCATION 1..489

; SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

US-10-335-977-4490
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4492, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4490:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                       NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-335-977-4492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4491, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUINITE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUINITE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 ACTICAAGAICAAGAIAAGAAAAGCCAAGAAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             642 acacaaagaacaagacaagcaaggcaaagg 673
                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/335,977
PILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
PRIOR APPLICATION NUMBER: 08/993,002
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 3GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...963
; SEQUENCE DESCRIPTION: SEQ ID NO: 4492:
US-10-335-977-4492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10031
CORRESSONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKTELD
STREET: 26 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                   COUNTRY: USA
ZIF: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 4492:
SEQUENCE CHARACTERISTICS:
LENGTH: 963 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
CITY: Boston
STATE: Massachusetts
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8154 aaaacraaaaracaaacraaaccaaarccacraaccaarrirraaaaaaarcacraaa 8095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8094 AATACTTAAAACAAAAAAAACTTATATTCAACGCAAAACTAATTATACTATAATACTAC 8035
                                                                                                                                                                                                                                                                                 126 TCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATGGCAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8034 Trrcaciradadadartriradcirccirccaacradadaarartriaci 7979
                                                                                                                                                                                                                              6 AAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAAATCAAAAGAAGCCCCAAGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 TGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCT 241
                                                                                                                                                                                0; Gaps
                                                                                                                         Query Match 9.7%; Score 39.2; DB 15; Length 17869; Best Local Similarity 47.9%; Pred. No. 2.5; Matches 113; Conservative 0; Mismatches 123; Indels 0;
; NAME/KEY: unsure
; LOCATION: 3465, 3586
; COTHER INFORMATION: n is a or g or c or
US-10-311-455-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 22, 2004, 17:14:09 Job time : 347 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: DEFENBROCK, Christian
APPLICANT: DEFENBROCK, Christian
TITLE OF INVENTION: Orytosine methylation
FILE REPERBNCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PLILING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-30
PRIOR SEQ ID NOS: 2424
SEQ ID NO 78
LENGTH: 17869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 CAÁTGAAACTAATCCTACAGAAGAAAAAAGTTAGAGCCAACGCCTAAATTAGAAGAAAA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 CAAGAAAGGAAACCCAGATGAGGAAAGAAAACGGCAGGAAATGACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.7%; Score 39.2; DB 13;
Best Local Similarity 64.1%; Pred. No. 0.65;
Matches 59; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 ACTTCAAGATCAAGATAAGAAAAGCCAAGAAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 ACACAAAGAACAAGACAAGCAAGGCAAAGAAG 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...966; SEQUENCE DESCRIPTION: SEQ ID NO: 4491: US-10-335-977-4491
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                          APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
NAME: MARITRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHERICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 4491:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -455-78/c
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Sequence Seq

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Length 7218;
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US-08-232-463-14/c
| Sequence 14, Application US/08232463
| Patent No. 5670367
| GENERAL INFORMATION:
| APPLICANT: DORNER, F.
| APPLICANT: SCHEIFLINGER, F.
| TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
| TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: FOLEY & Lardner
| STREET: 1800 Diagonal Road, Suite 500
| CITY: Alexandria
| STATE: VA
| COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMINY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-09-071-224-3
US-09-071-224-3
US-08-659-188-9
US-08-655-227-9
US-08-655-227-9
US-09-149-976-9
US-09-149-976-9
US-09-38-326-9
US-09-38-326-9
US-08-098-3278-41
US-08-098-3278-41
US-08-088-3278-41
US-08-088-3278-41
US-08-088-3278-41
US-08-088-3278-41
US-08-088-3278-41
US-08-088-3278-38
US-08-088-3278-38
US-08-098-3278-38
US-08-098-3278-38
US-08-098-3278-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
RICOR APPLICATION: 435
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 49;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      31940
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Appl
Sequence 1567, Ap
Sequence 1, Appl
Sequence 16, Appl
Sequence 173, Appl
Sequence 1733, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212, App
212, App
212, App
21, App
11322, Ap
151, App
1151, App
1142, Ap
8, Appli
1190, App
465, App
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1161, Ap
32, Appl
5, Appli
                                                                                                                                                                                   (without alignments)
2809.439 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                      1 atgggaaattatctcctgcg......atgaagttgtgtttccacac 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Sequence
Sequence
                                                                                                                                                           April 22, 2004, 13:49:27; Search time 80 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:*

(GGTZ 6/ptodata/2/ina/5A COMB.seq:*

(GGTZ 6/ptodata/2/ina/5B_COMB.seq:*

(GGTZ 6/ptodata/2/ina/6A_COMB.seq:*

(GGTZ 6/ptodata/2/ina/6A_COMB.seq:*

(GGTZ 6/ptodata/2/ina/PCTUS COMB.seq:*

(GGTZ 6/ptodata/2/ina/PCTUS COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14
US-09-328-352-1567
US-09-107-523A-2987
US-09-904-615-16
US-09-914-615-16
US-09-134-0016-1153
US-09-134-0016-1161
US-09-134-0016-1161
US-09-134-0016-1161
US-09-134-0016-1161
US-09-134-0016-1161
US-09-131-962A-5
US-09-131-962A-5
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US-09-131-962A-5
US-09-131-962A-5
US-09-131-962A-5
US-09-131-962A-5
US-09-131-962A-5
US-09-131-122-21
US-09-108-09-1142-1122-21
US-09-611-976-1324
US-09-611-976-1324
US-09-611-976-1324
US-09-611-976-1324
US-09-611-976-1324
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US-08-956-171E-4053
US-09-620-405B-465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                 US-10-005-907-1_COPY_25_429
405
                                                                                                         - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                     IDENTITY NUC Gaport 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                           OM nucleic
                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                           Run on:
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Sequence 1, Application US/08545528D
Patent No. 6537773
GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome,
Patent No. 65377773
TITLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 AAGCAATTACACCATCTGAAAATAAGCAATTAGAAGTGCACCAAGTTCAAGAATAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 CCACTICIAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAGTGTGTCACACTGTCA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAAGCCAAGAAGTTTCAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 Troccanciarrangeacrocconnantananangeaccacangeaccanananangec
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50.0%; Pred. No. 0.072;
tive 0; Mismatches 92; Indels
  THERAPEUTICS CORPORATION
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-040-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/01571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...549
SEQUENCE DESCRIPTION: SEQ ID NO: 2987:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                 COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                       STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 2987:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                   COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: UG/09/328,352
CURRENT PILLING DATE: 1999-06-04
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                  127 CAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATGGCAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                247 AGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGACAGTTT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 ACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 ACGGTAGAAAGACAATACTTGGGGCAAATGGATATGTTCAAAGAACCATGCCCCAATACT 196
                                                                                                                                                                                        187 GGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 AATAATTAGAAAACCAATAAACCAGGCTTCAGAGGTGATAACCCACGGGTGTAAATGGGT
                                                                     7 AATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAAATCAAAAGAAGCCCAAGAAAGGA
                            Gaps
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---- 73; Indels
                            Indela
ilarity 2.2%; Pred. No. 4e-05;
Conservative 192; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 GCTCATTAAAAGAAATTGGCTGCAAGACAGAACA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.2; Di
Pred. No. 0.03'
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2987, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1147 RRRRRRRRRRRRRRRRR 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1567, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AGAGAAAGGTCAGAGACAGAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Acinetobacter baumannii
US-09-328-352-1567
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.9%;
Matches 82; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1567
  Best Local Similarity
Matches 7; Conserv
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US-09-107-532A-2987
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                       97 AIGACTACATTIGAAAGAAAACTICAAGAICAAGATAAGAAAAAGCCAAGAAGTTICAICC 156
                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                   15 CCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGA
                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                          Query Match 9.0%; Score 36.4; DB 4; Length 580073; Best Local Similarity 51.9%; Pred. No. 2.4; Matches 82; Conservative 0; Mismatches 76; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 ACTICIAAICAGGAAACGAGAAIGGCAGIGGIICIGA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6566325

Fatent No. 6566325

FAREAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REPERENCE: 22032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
FRIOR APPLICATION NUMBER: 09/511,554
FRIOR APPLICATION NUMBER: 09/511,554
FRIOR APPLICATION NUMBER: 60/097,917
FRIOR APPLICATION NUMBER: 60/097,917
FRIOR FILING DATE: 1998-08-25
FRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 16
LENGTH: 2608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                           CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH: 580073
                                                                                                                                                                                             TYPE: DNA ORGANISM: Mycoplasma genitalium
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Best Local Similarity 54.1
Matches 72; Conservative
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US-09-904-615-16
FILE REFERENCE: PB193P1
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US-09-904-615-16
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709,2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 CTCCCTCACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCT 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 TTCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAA
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APPLICANT: Racie, Lisa A.

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

APPLICANT: Spaulding, Vikki

APPLICANT: Spaulding, Vikki

APPLICANT: Spaulding, Vikki

APPLICANT: AGOSTING, Michael J.

ITILE OF INVENTION: ENCODING THEM

NUMBER OF SEQUENCES 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Ingrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.6%; Score 35; 48.3%; Pred. No.
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Sequence 1733, Application US/09540236
Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09014969
Patent No. 5965397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.3
Matches 98; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: M.catarrhalis
US-09-540-236-1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 KYRRRRRRAMWWWKSMCWWKKSKSWWRSWGWMTKRWKGRGAASWAGYMSWMTYMTRWRY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ** :::|::|::|::|::|
WMYYWMARRITWWGWRASCYRGAYWASAGMYYWWMYYWWRRRKWMYSAGWSWWRKWTRRCAS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCTC 242
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                                                                                                                                                                                                                                                                                                17 TGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGATG
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12.4%; Pred. No. 0.26;
ative 110; Mismatches 102; Indels
                                                                                                                                                                                                                         Score 35; DB 2; Length 2447;
Pred. No. 0.52;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 AAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8976, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: STS and Encoded Human Proteins.
TILE REFERENCE: GENSET.054FR2
CURRENT FILLION DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 110;
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                               8.6%;
ilarity 50.9%;
Conservative
                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-621-976-8976
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Best Local Similarity
Matches 83; Conserv
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YY 283
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MOLECULE TYPE:

US-09-014-969-14
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Best Local
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GENERAL INFORMATION:

APPLICANT: LYAID DOUGETEE-Stamm et al

APPLICANT: LYAID DOUGETEE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLECT ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICANCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ACTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 TCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAAT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 ccarcaaargragaaararraragrgaagrrrrgaggarrragaggaagrargagrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REPERENCE: UX01523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR PLING DATE: 1999-02-03
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 118067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.8; DB 4; Length 729; Pred. No. 0.34; 0; Mismatches 92; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34.8; D
Pred. No. 3.5;
0; Mismatches
Sequence 1161, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; CRAPHYLOCOCCUS epidermidis US-09-134-001C-1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
? Patent No. 6605432
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.5%;
Matches 90; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.7%;
Matches 72; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA 539
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303 GITTAGAGAAAGGICAGAGACAGAATAIGCCCTTCTTAGGACTICTGTTAGTAGGCTTG 362
                                                                                                                                    481 Grigagropagegropaacceacaacarenteacearrogracirecreaagecares 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
IILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IILLE OF INVENTION: Asids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REPERENCE: 10.466.14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PRIOR DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PRIOR DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-06

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

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PRIOR FILING DATE: 1999-11-30

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PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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                                                                                                                                                                                                                                                 TGACCACACTCGTGAGCA 404
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Ither, Jennie P.
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Ashkenazi, Avi
Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                            US-09-907-794A-212
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  97 ATGACTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCC 156
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTY: UNITED STATES OF AMERICA
ZIP: 19998
COMPUTER READABLE PORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: MINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
APPLICATION NUMBER: US/09/133,962A
FILING DATE: 14-Aug-1998
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION MUMBER: U.S. 07/977,339
FRIENG DATE: 17-MOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 34; DB 4; Length 1462;
ilarity 52.9%; Pred. No. 0.83;
Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHN JOSEPH OKULEY

TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID
DELTR-12 DESATURASES AND RELATED
ENZYMES FROM PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1043-D
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JONATHAN EDWARD LIGHTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 108..1247
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-133-962A-5
                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09133962A
Patent No. 6372965
GENERAL INFORMATION:
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TELEPHONE: (302)992-5481
TELEFAX: (302)773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
IMMEDIATE SOURCE:
CLONE: pSF2-165K
                                                                                                                                                                                                                     117290 AATTTGCAAAAGA 117277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                 157 ACTTCTAATCAGGA 170
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ORIGINAL SOURCE:
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Best Local Similarity
Matches 73; Conserv
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-09-133-962A-5/c
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243 CCTGAGCTCCAATGATGATGACTATGAGAACATTGACTCCCTCACAAGGAAAGTGAGACA 302

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APPLICANT: Williams P. Mickey
TITLE OF INVENTION: Scretted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION UMBER: US/09/905,125A
CURRENT PILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                            DB 4; Length 1985;
                                                                                                                                                                                                                                                                                                                                                 70; Indels
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Pred. No. 0.95;
0; Mismatches
                 PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1944 AAAAAAAAAAAAAAAAAAAAA 1969
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Application US/09905125A
6664376
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.1%;
Matches 76; Conservative
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lvaroff, Ellen
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Mather, Jennie P.
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                                                                                                                                                                                                                      TYPE: DNA
CAGANISM: Homo sapiens
US-09-907-794A-212
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2 TGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAAGAATCAAAAGAAGCCCAAGA
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Pred. No. 0.95;
0; Mismatches 70; Indels
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-02
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PRIOR PELLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-03
PRIOR PELLING DATE: 1999-12-03
PRIOR PELLING DATE: 1999-12-03
PRIOR PELLING DATE: 1999-12-03
PRIOR PELLING DATE: 1999-12-04
PRIOR PELLING DATE: 1999-12-04
PRIOR PELLING DATE: 1999-12-04
PRIOR PELLING DATE: 1999-12-05
PRIOR PELLING DATE: 1999-12-05
PRIOR PELLING DATE: 1999-12-05
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PRIOR PELLING DATE: 1999-12-05
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.1%;
Matches 76; Conservative
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Grimaldi, Christo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA; ORGANISM: Homo sapiens
US-09-905-125A-212
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Pred. No. 0.95;
0; Mismatches 70; Indels
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**PRIOR PILLING DATE: 1999-12-16

**PRIOR PILLING DATE: 1999-12-20

**PRIOR FILLING DATE: 1999-12-20

**PRIOR FILLING DATE: 1999-12-20

**PRIOR FILLING DATE: 2000-005

**PRIOR FILLING DATE: 2000-005

**RIOR FILLING DATE: 2000-005

**SEQ ID NO 212

**SEQ ID NO 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER: PCT/US99/21547
ILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                G DATE: 2001-07-10
TION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLICATION NUMBER: PCT/US99/20594.
LING DATE: 1999-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICATION NUMBER: PCT/US99/20944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/145,698 PILING DATE: 1999-07-26 APPLICATION NUMBER: US 60/146,222 FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-02-22
APPLICATION NUMBER: US:60/143,048
FILING DATE: 1999-07-07
                                                                                                                                                           illiams, P. Mickey
ood, William, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4%;
                                                                                                          tewart, Timothy A.
                                                                       Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .999-09-13
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 76; Conserv
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62

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2 TGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGA

15

RESULT

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1 ATGGGAAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAG 60
                                                                                 APPLICANT: Greiner, Beate
APPLICANT: Unger, Eberhard
APPLICANT: Gorbe, Gislinde
APPLICANT: Gorbe, Gislinde
TITLE OF INVENTION: OLICONUCLEOTIDES FOR THE INHIBITION OF HUMAN eg5
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 0.2491.678
CURRENT APPLICATION NUMBER: US/09/627,122
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: SA40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 5340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.8; DE Pred. No. 1.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 22, 2004, 16:09:14 Job time : 86 secs
Sequence 21, Application US/09627122
                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-627-122-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 49.7%;
Matches 86; Conservative
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April 22, 2004, 18:31:30 ; Search time 2076 Seconds (without alignments) 8455.650 Million cell updates/sec
                                                                                                                              US-10-005-907-1_COPY_25_429
405
1 atgggaaattatctcctgcg......atgaagttgtgtttccacac 405
                                                                                                                                                                                                                                                            3364370
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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em_htgo_mus: *
em_htgo_other: *
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em_htg_hum:*
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em_pl:*
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ggb_intg.*

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ggb_bh.:.*

ggb_ri.**

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ggb_gri.**

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ggb_gri.**
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em or:*
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Maximum DB seq length: 405
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                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                  Searched:
                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

cription	S75319 12S rRNA {n G37943 C4M29 Plasm RV014350 S208P6381	AF351282 Gossypium BD211954 Novel hum	AL395108 T3 end of L17710 Human STS U	AY198661 Arabidops 1,18521 Human chrom	AR417479 Sequence	AJ566324 Ficus syc	BC015361 Homo Bapi G47173 Z15801 1 Ze	AL395173 T7 end of	Ars4304/ Mesoburnu G50943 SHGC-78669	AY040769 Mus muscu	AFI16644 Homo sapi	Ak413685 Sequence BD109238 EST and e	X94294 P.falciparu	BD109240 EST and e	AY376246 Homo sapi	L31114 Human STS U	AJ276787 Acrocepha	AR357935 Sequence	AF201952 Plasmodiu aX185675 Sectionse	BV077053 S210P6110	AY054826 Plasmodiu av054852 Plasmodiu	BV095162 RPAMMSEQ0	AX435334 Seguence	D67094 Hepatitis v	L12269 Homo sapien	272 P.I 10859 E	Rattus n Determi		linear MAM 27-MAY-1995	repeat macrosat , fibroblasts, G		Vert	a; Felidae; and O'Brien
	S7531 1 G379	A AF351282 6 BD211954	1 CNSC	AY198661	AR417479		9 BC015361 11 G47173		AF543047 G50943						AY376246	HUMUT51		AR357935		н		н		4	1	PFAMAD AF31085	10 RNU00763 6 BD244367	ALIGNMENTS	372 bp DNA	ne pNumt cats, l		Chordata; Craniata;	Carnivora; Fissiped , Masuda,R., Modi,W
	3 239	2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	.1 263	.8 270	9 6 6	.5 277	.5 372	.4 353	.4 401 .4 230	296	. E.	.3 249 249	.3 385	.2 240	.2 190	.2 288	.2 357	1 400	4.0	. 0.	۰.۰	. 0.	0.0	. 0	6	ס ס				{nuclear tus=domes	9 9.1 GI:83395	catus (cat) catus yota; Metazoa	malia; Eutheria; (bases 1 to 372) ez,J.V., Yuhki,N.
Score	1 1 1 1	37.	36,	35.		 4 4	9 8 4 4	, m	ы	2 3		 	. m	 	99	 	33.	חיח	32	3 6	32.	3.5	32	. 6	m	3,3	 			Z	SION S75319 ON S75319.1	URCE Felis catus ORGANISM Felis catus Eukaryota;	
ag X	1	מ מ	97	α, σ	. 51	c 12	E. I. I.	127	17	ο 182	525	22		25	0 26	2 6	0	4 E	m r	ე გ.გ.	:	o O	m r	Ω υ 4.	4	4. 4	0		RESULT 1 S75319 LOCUS	DEFINI	ACCESSION VERSION KEYWORDS	SOURCE ORG	REFERENCE AUTHORS

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Gaps

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BV014350 375 bp DNA linear STS 30-MAY-2003 S20896381FF2.T0 129S1/SvImJ Mus musculus STS genomic, sequence tagged site.
BV014350.1 GI:31098245
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Made, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCv3 C57EL/GJ assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 CTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                               Score 41.6; DB 11; Length 239;
Pred. No. 5;
0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                          /clone lib="plasmodium falciparum haploid"
/dev stage="erythrocytic haploid stage"
1. .239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 CTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 ATABABABABABABABABGGGGGGTAGGGGAAGAGT 215
                                                                                               Location/Qualifiers
1. 239
/organism="Plasmodium falciparum"
/orjanism="Plasmodium falciparum"
/dol_type="genomic DNA"
/strain="HB3xDd"
/db_xxef="taxoni5833"
/map="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kersli@genome.wi.mit.edu
Primer A: None
                                          10 mM Tris HCl, pH 8.3
1.5 mM MgCl2
50 mM KCl.
                                                                                                                                                                                                                                                                                                                                     complement (221. .239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                 ch 10.3%;
1 Similarity 53.8%;
86; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer B: None
STS size: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12466852
                                                                                                                                                                                                                                                                                                     primer_bind
primer_bind
ORIGIN
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Best Local S:
Matches 86
                                                                                                                              source
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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BV014350
                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 CCAAAAAAAGTTAGGTCAAGGTGTAGCTCATGAGATGGGAAGCAATGGGCTACACTTTCT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 AAATGACTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 CCACTTCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCA 214
      mitochondrial
                                                                                                      GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 160474] from the original journal article. This sequence comes from Fig. 6B. Map location: D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
I (bases 1 to 239)
Su,X.-z., Ferdig,M.T. and Wellems,T.E.
Integrated genetic and physical maps of Plasmodium falciparum
Unpublished (1999)
On Mar 6, 1999 this sequence version replaced gi:3056687.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial heat: 2min at 94oC
Cycles: 30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
Machine: Perkin Elmer GeneAmp 9600
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bidg. 4, Room 126, NIH Campus, Bethesda, MD 20892-0425
Tel: (301) 496-4021
Fax: (301) 402-0079
Email: Lew@helix.nih.gov
Primer A: TCTTCACTTTTGTCCATCAT
Primer B: CATTGGTACTGTAGTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-10 ng
5 pM each
0.3 ul of 10 mM stock solution
0.5 unit
15 ul
                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 372;
Numt, a recent transfer and tandem amplification of 10Ms to the nuclear genome of the domestic cat J. Mol. Evol. 39 (2), 174-190 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                                                                                                                                                                                                                                                                                                               Score 43.2; DE
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                          1. .372
/organism="Felia Catus"
/mol_type="genomic DNA"
/db_tref="taxon:9685"
1. .372
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Thomas E. Wellems
                                                                                                                                                                                                                                                                                                                   gene="12S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer:
dNTPs:
Tag Polymerase:
Total Volume:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 TTAATCACATCCCCCA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 AAAATTAGAATACCCA 305
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.4%;
Matches 78; Conservative (
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G37943.2 GI:4337400
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                   gene
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                                                                                    PUBMED
                                                                                                                                                                                           FEATURES
                                                                                                        REMARK
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G37943
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DRMANAC,
RADOMIR CRKVENJAKOV, WARK DICKSON, SNEZANA DRYANAC, IVAN LABAT,
RADOMIR LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
BIRJIT STACHE CRAIN
CIZNIS/09, CIZNIS/09, CO7K14/47, CO7K14/82, CO7K16/18, CIZNI/15, PC
                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 281)
Milliams, L.T., Becobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S.,
Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D.,
Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,
and Crain, B.S.
                                                                                                                                                                                                                                       PAT 17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 02-JUL-2002
PF 28-JAN-1999 JP 2000556580
RE 28-JAN-1999 US 60/075954 PR 28-JAN-1999 US 60/075954 PR 28-JAN-1999 US 60/075954 PR 31-MAR-1998 US 60/080666,21-OCT-1998 US 60/080515 PR 63-APR-1998 US 60/080666,21-OCT-1998 US 60/105234 PR 28-OCT-1998 US 60/105877
PI LOUIS T WILLIAMS,JAIME ESCOBEDO,MICHAEL A INNIS,PABLO PI DOMINGUEZ GARCIA,
PULLIS SUDDUTH KLINGER, CHRISTOPH REINHARD,KLAUSE GIESE,FILIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 CTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 apataaangnaaaaagaannanaacaananaaanaaagagntnanaaanaaanaaaat 136
                     81 AAGAAAACGGCAGGAAATGACTACATTTGAAAGAAAAACTTCAAGATCAAGATAAGAAAAG 140
                                                      GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CI2N1/21, C12N5/10, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC A,T,C or G
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0
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                                                                                                                                                                                                                          Novel human genes and gene expression products 11.
BD211954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and gene expression products ii
Patent: JP 2002519000-A 96 02-JUL-2002;
CHIRON CORP, HYBED INC
OS Homo sapiens (human)
PN JP 2002519000-A/96
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Best Local Similarity 42.9%; Pred. No. 66;
Matches 66; Conservative 0; Mismatches
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Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                             BD211954.1 GI:33021724
                                                                                                                                                                                                                                                                                                              JP 2002519000-A/96.
Homo sapiens (human)
Homo sapiens
                                                                                                  141 CCAAGAAGTTTCAT 154
                                                                                                                                        115 GGAAGGAGCTTCGT 102
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Gossypium hirsutum

Eukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

Reddy,U.K., Pepper,A.E., Abdurakhmonov,I., Saha,S., Jenkins,J.,

Brooks,T.D. and El-Zik,K.M.

New dinucleotide and trinucleotide microsatellite marker resources for cotton genome research

Unpublished

Reddy,U.K., Pepper,A.E., Abdurakhmonov,I., Saha,S., Jenkins,J.,

Brooks,T.D. and El-Zik,K.M.

Brooks,T.D. and El-Zik,K.M.
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the strain from which the particular read came. The validation of for these SNPs was estimated at approximately 98%.

Location/Qualifiers
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Gossypium hirsutum clone JESPR41 microsatellite sequence.
AF351282
                                                                                                                                                                                                                                                          Length 375;
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                                                                                                                                                                                                                                                                                                 Indels
                                                    1. .375
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/db_xref="taxon:10090"
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/clone lib="12951/SyImJ"
                                                                                                                                                                                                                                                       9.8%; Score 39.8; DB 11;
52.0%; Pred. No. 14;
ilve 0; Mismatches 82;
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/mol type="genomic DNA"
/strain="Tamoot Sphinx"
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College Station, Texas 77843, USA
Location/Qualifiers
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/note="microsatellite"
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Matches 89; Conserv
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (Dases I to 404)

E 1 (Dases I to 404)

E 2 Gerken, S.C., Matsumani, N., Lawrence, E., Carlson, M., Moore, M., Ballard, L., Matsumani, N., Lalouel, J.-M. and White, R. Tingey, A., Rodriguez, P., Albertsen, M., Lalouel, J.-M. and White, R. Genefic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome

L Unpublished (1993)

Original source text: Homo sapiens DNA.

Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics

Salt Lake City, UT 84112

Salt Lake City, UT 84112
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AY198661.1 GI:27894615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 GGGAGAGAGAATCAAAAAGAAGCCCCAAAGAAAGGAAAACCCCAGATGAGGAAAAGGGCAGGA
96 AATGACTACATTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AGAAANAAAGAAAGAAANNNAAAAGGAAAGAAAAGGAAAAGGAAAAGAAAAG
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                                                                                                                                    HUMUT5151 404 bp DNA
Human STS UT5151, sequence tagged site.
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Best Local Similarity 56.2%; Pred. No. 90;
Matches 63; Conservative 0; Mismatches
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/standard_name="STS UTS151"
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/db_xrefe"taxon:9606"
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PCR Cycles: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail: sts@corona.med.utah.edu
Primer A: CATGAGCCAAGATTGTGCC
Primer B: AAAATGCTGTAATTACAGGCG
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Extension: 72C 20sec
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                                                                                                                                  CNSO6EHA 11near STS 10-JAN-2001 T3 end of clone AROAA021E11 of library AROAA from strain CBS 732 of Zygosaccharomyces rouxii, sequence tagged site.
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de Montkgny, J., Straub, M., Potier, S., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Souciet, J.,
Genomic exploration of the hemiascomycetous yeasts: 8.
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/mol_type="genomic DNA"
/strain="CBS 732"
    135 AAANNCAAGNTANAAANNATGNTAACNANNGTGA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zygosaccharomyces rouxii
FEBS Lett. 487 (1), 52-55 (2000)
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/clone lib="AROAA"
/note="end : T3"
1. .263
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="22"
                                                         Initial Denaturation: 94C 300sec
PCR Cycles: 5
Denaturation: 94C 10sec
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/wol_type="genomic DNA"
    Primer B: AAGATTATTGGCACCAAAACC
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complement (317. .337)
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Extension: 72C 20sec
                       32P-label: A Primer PCR Profile:
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(acken, S.C., Mateunami, N., Lawrence, E., Carlson, M., Moore, M., Tingey, A., Rodiguez, P., Albertsen, M., Lalouel, J.-M. and White, R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome

Unpublished (1993)

Original source text: Homo sapiens DNA.

Submitted by: Utah Center for Human Genome Research University of Utah. Dept. of Human Genetics

2160 Eccles Institute of Human Genetics

Salt Lake City, UT 84112

e-mail: sts@corona.med.utah.edu

Primer A: TGCCACTGAACTCCAGCTT
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              Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tracids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 270)

May, B.P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,
Arabidopsis genomic sequences flanking Ds enhancer and gene traps
in transgenic lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 CAAAAATTGAĞTTCCTTTAACAAGATCATAATCGTAACACAAATCCAAAGCCCAAAGAT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAGAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                               Submitted (17-DEC-2002) Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA http://genetrap.cshl.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118521.1 GI:308187
STS; PCR primer; STS sequence; microsatellite marker;
microsatellite repeat; repeat polymorphism; sequence tagged site;
tetranucleotide repeat.
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McCombie, N.W., Simorcwski,J., Arroyo,J.-M., Vaughn,M.W., Shen,R.,
McCombie, W.R. and Martienssen,R.A.
Direct Submission
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Pred. No. 1.7e+02;
0; Mismatches 79; Indels
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Human chromosome 22 STS UT5116, sequence tagged Bite.
118521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAAAAACCCTACAGAAATTGCAAAAAGTAAAAAGGAGAAT 219
                                                                                                                                                                                                                                                                                                                                                                                                                       /organiem="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="TT2091.Ds3.02.07.00.b.270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ecotype="Landsberg"
/note="transgenic line ET2091"
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Best Local Similarity 51.2%;
Matches 83; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATGG 182
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1 (bases 1 to 399)

Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
Edwards,J.-B.D.M. in Jobert,S. and Biordano,J.-Y.
Patent: US 6639063-A 8976 28-OCT-2003;
Mg++: 1mW
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 4.
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8.6%; Score 34.8; DB 6; I
Best Local Similarity 12.4%; Pred. No. 2.6e+02;
Matches 30; Conservative 110; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                         Query Match
8.6%; Score 34.8; DB 11;
Best Local Similarity 52.0%; Pred. No. 2.6e+02;
Matches 78; Conservative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 bp DN Sequence 8976 from patent US 6639063.
                                                                                                                                                                                                      43. .337
/standard_name="STS UT5116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 CACTICIAAICAGGAAAACGAGAAIGGCAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 GGCAGGCAGGTGAGAGCGAGGAAGGAAG 271
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PLN 30-JUN-2003

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Direct Submission
Submitted (28-MAY-2003) Dawson D.A., Department of Animal and Plant
Sciences, University of Sheffield, Alfred Denny Building, Western
Bank, Sheffield, S10 2TW, UNITED KINGDOM
Location/Qualifiers
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microsatellite; repetitive DNA.
Ficus sycomorus
Ficus sycomorus
Ficus sycomorus
Ficus youngiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Moraceae; Ficus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 372)
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Submitted (01-0CT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                         Dawson, D.A., Ahmed, S., Compton, S.G., Gilmartin, P.M. and Burke, T. Isolation of microsatellite loci in the fig, Ficus sycomorus Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="microsatellite
rpt_unit: [T)6 (G)1 (T)6 (G)1 (T)7 (A)2 (TTTC)1 (TTTC)1
(TTTC)5 (TTTC)7 (C)1 (T)18"
/rpt_type=TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 8.5%; Score 34.6; DB 8; Length 277; Similarity 58.1%; Pred. No. 3.18+02; 61; Conservative 0; Mismatches 44; Indels (
                                                                     FSY566324 linear 277 bp DNA linear Ficus sycomorus microsatellite DNA, clone FIGT09D12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 GACTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
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Homo sapiens, clone IMAGE:3886095, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Ficus sycomorus"
/mol_type="genomic DNA"
/mol_tref="taxon:182129"
/clone="rIGT09DD12"
87. .190
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BC015361.1 GI:15929880
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E dwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

In Patent: JP 2002010789-A 5109 15-JAN-2002;
GENSET CORP.

OS Homo sapiens (human)

PN JP 2002010789-A/5109

PD 15-JAN-2002

PP 07-AUG-2000 JP 200280989

PR 05-AUG-1999 US 60/147499

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
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183 CAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCTC 242
                                                                       C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
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                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                DNA

    .399
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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EST and encoded human protein.
BD113032.
BD113032.1 GI:23207850
JP 2002010789-A/5109.
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Matches 30; Conserv
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282 YY 283
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Gaps

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98

PRI 04-OCT-2001

linear

84

1.5 mM 50 mM 10 mM 8.3.

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JS3 bp DNA linear STS 10-JAN-2001 T7 end of clone AROAA022A02 of library AROAA from strain CBS 732 of AL395173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—Whotor: Milynpin with added BstXI site; V-type: Phage; Genomic DNA from a single adult Zebrafish of AB strain was digested with Alul, Caceli, Haelli, NlaVI, or Rsai. Fragments in the range of 250-500 bp were gel purified and a BstXI linker was added. The fragments were cloned into a modified Milynpin vector and transformed close Coli Mislapha. Microsatelllite sequences were screened with labeled d(A)15 and d(GI)15 oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 ATGAGAACATTGACTCCCTCACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
Zygosaccharomycetaes; Zygosaccharomycetes;
Saccharomycetales; Saccharomycetaes;
Zygosaccharomyces.

1 (bases 1 to 353)
Souciet.J.I., Artiguenave,F., Blandin,G.,
Bolotin-Eukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 gigigiterririagircricraargaaagiragagarrirgaaacaarcraggercagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 ACACTGTCATTAATCACATCCCCCATCAGAGATCCTCCCTGAGCTCCAATGATGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
8.5%; Score 34.4; DB 11; Length 397;
Best Local Similarity 52.9%; Pred. No. 3.3e+02;
Matches 74; Conservative 0; Mismatches 66; Indels 0;
72 degrees C for 1.5 minute
27
MJ Research PTC-100
                                                                                     10 ng
each 375 nM
each 200 uM
0.034 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="Zebrafish AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'dev_stage="Adult"
'lab_host="DH5alphaF'IQ"
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
| strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:7955"
clone="215801"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (289. .308)
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      Polymerization:
PCR Cycles:
Thermal Cycler:
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Total Vol:
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CNS06EJ3
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                       DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site:

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

I (bases 1 to 397)
Ziniti, J., Jackson, D. G. and Fishman, M. C.
A Zebrafish microsatellite map
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LiML at: http://image.llnh.gov Series: IRAK Plate: 22 Row: c Column: 19. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 14941004, 149 13th Street, Charlestown, MA 02129, USA
Fax: 617765806
Email: fishmanemgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: CGCCAAGTACCCAAAATAA
Primer B: AGCGTTTTCTTCCAGTCCAA
STS size: 223
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGGCCCAAGAAAGGAA
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         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3886095"
/tissue_type="Lung, carcinoma, large cell
undifferentiated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for 5.0 minutes for 1.0 minute for 1.0 minute
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 AAAAAAAAAAAAAAAAAA 371
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Danio rerio
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencage, cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequesosoope.cns.fr. - Web: www.genescope.cns.fr)

This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazii, Zygoaaccharomyces rouxii, Saccharomyces ervazzii, Zygoaaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hassenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCCAAGAAAGGAAACCCAGATGAGGA 80
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemisacomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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de Montigmy,J., Straub,M., Potier,S., Tekaia,F., Dujon,B.,
Wincker,P., Ariguenave,F. and Souciet,J.
Genomic exploration of the hemiascomycetous yeasts: 8.
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8.4%; Score 34.2; DB 11; Length 353;
Best Local Similarity 54.3%; Pred. No. 3.8e+02;
Matches 69; Conservative 0; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zygosaccharomyces rouxii"
/mol_type="genomic DNA"
/strain="CBS 732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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141 CCAAGAA 147 || || 273 AAAAAA 279

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Search completed: April 23, 2004, 03:08:42 Job time : 2081 secs

OM nucleic

Run on:

Sequence:

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Database

Result Š.

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A2273050 RPCC-23-8
CE32306 Ltgr-ggs-
A2419893 1M0196A08
A2419893 1M0196A08
A1725744 AL725744
AL725744 AL725744
AL725744 AL725744
AL725744 AL725744
AL73571 Terrandon
AL118961 Terrandon
AL118961 Terrandon
AL13817 AU039357
AL034047 DEOSOPhil
CE34364 Ltgr-ggs-
CE345319 nC23h08.8
CE462660 Ltgr-ggs-
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BG491777 6G23409.w
BG4981526 MR3-CN014
BG497771 6G25400.w
BG4981526 HR3-CN014
BG497771 6G25400.w
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CE35890 Ltgr-ggs-
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CE377846 Ltgr-ggs-
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BM15509 Ltgr-ggs-
CE37881 BC-05-
BM15508 NACL-05-
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CF544822 lad83b08.
BE291389 BE291389
CF804314 lad70c09.
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1 (bases 1 to 288)

1 (bases 1 to 288)

2 Eatherikrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackerbush, J. and Keele, J.W.

Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly

22213789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 436
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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BG382689
BG382689
B1671449
B1671449
CM22569
BM361846
CM797746
CM30727
CM30727
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CN02022W
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Sus scrofa
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                                                                                      April 22, 2004, 18:29:17; Search time 2022 Seconds (without alignments) 5981.297 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AY404587
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                                                                 - nucleic search, using sw model
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Match Length DB
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353
259
203
                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 405
                                                                                                                                                                                                                                                                                                                                                                                      EST:*
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11.6
11.5
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46.8
6.64
44.4
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                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                Scoring table:
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<li..>353
/gene="GCET2"
/locus_tag="HCM1940"
                                                                                        Query Match
Best Local Similarity 47.7%;
Matches 106; Conservative (
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CE192340/c
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Pan troglodytes GCET2 gene, VIRTUAL TRANSCRIPT, partial sequence,
avanates
                                                                                                                                                                                                                                                                                                                                                                                                                   ä
v0.980904.e. Vector identified by cross match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 CACAAGGAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGCCCTTCTTAGGAC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GACTTACACTCCAAGTTTTTCTTCCTATACCCCTGAGAATGATTATGAACTTGTGCTTCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. 1 (bases 1 to 353)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritara, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9823"
/db_xref=rtaxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC_2PIG"
/note="Vector: pGNV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 TICTGITAGI --- AGGCCTIGITCCTGCACCCATGAGCATGATGAAGTTGTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 353)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                                                                                                                                             Length 288;
                                                                                                                                                                                                                                                                                                                                                                           16.0%; Score 64.8; DB 10; Length illarity 75.8%; Pred. No. 4e-05; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                    organism="Sus scrofa"
                                                    FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 19 row: F column: 21
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes (chimpanzee)
Pan troglodytes
          and -minmatch 12 options.
PCR PRimers
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Best Local Similarity
Matches 94; Conserv
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AY404587
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Ligr-gss-dog-17000371469886 Dog Library Canis familiaris genomic, genomic, genomic survey sequence.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Nockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
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                                                         7
                                                                                                                                                                 131 AAAGANNNAAGATTCCCAAAACGAAATGAAGGAATGTCATCNACTCCATCCAGNNNNN 190
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                                                                                                                                                                                                                                                                                    191 NNNNNNNNNNNNNNNNNNNNSÄGNÄGTGTGTGTTÄNÄNCNTCÄTCÄÄTNNNCGGGTTCTCTG 250
                                                                                                                                                                                                                                                                                                                                              231 TCAGAGATCCTCCCTGAGCTCCAATGATGATGGCTATGAGAACATTGACTCCCTCACAAG 290
                                                                                                                                                                                                                                                                                                                                                                                                    251 NACAAGGCCATCAGGGAACTCTGCTGAAGAGTACTATGAGAATGTTCCCTGCAAAGCTGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris
Eukaryota, Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metacoa; Chordata; Cranidae; Canidae; Canidae; Canidae; I (bases 1 to 259)
Kirkness, E. P., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                174 CGAGAATGGCAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACA---TCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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/organism="Canie familiaris"
/mol type="genomic DNA"
/strain="standard Poodle"
/db_xref="taxon:9615"
/clone libb="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral Blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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   Length 353;
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 GAGACCCAGAGAGCCCTTGGGAGGAACTGAGACTGAGTATTC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 GAAAGTGAGACAGTTTAGAGAAAGGTCAGAGACAGAATATGC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 11.5%; Score 46.6; DB 29;
Best Local Similarity 59.4%; Pred. No. 0.84;
Matches 79; Conservative 0; Mismatches 54;
Score 46.8; DB 29;
Pred. No. 0.77;
                                                         0; Mismatches 113;
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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 19106 EYRY cadex - France
BRail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10480.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?reeq=COAPF004ZG06ND1&cluster=10480.f. Contact :
Reng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAPF004ZG06NP1.
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Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, J., Tagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., MashU Stem cell EST Project
Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett
WashU, Human Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 20-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                  Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 404)

Liw Bu, Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 CGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGGAAAACCCAGATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 43.4; DB 13; Length 404; 55.0%; Pred. No. 5; Indels 0 tive 6; Mismatches 52; Indels 0
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labb9e12.y1 SiEP Mus musculus CDNA 5', mRNA sequence.
CF351413
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           .404
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Matches 7
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CF351413
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BX367419 Homo sapiens T CELLS (UURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens CND4009YM22 3-PRIME, mRNA sequence.

BX367419

BX367419.1 GI:30455633

EST.
                                                                                                                                                                                                                     בהשבים 203 bp DNA linear GSS 24-SEP-2003 tigr-ges-dog-17000359492028 Dog Library Canis familiaris genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 AAAGAAAACGGCAGGAAATGACTTTGAAAGAAAACTTCAAGATCAAGATAAGAAAA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
  107 TTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATC 166
                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria; Carnivora, Fissipedia, Canidae, Canis.

1 (bases 1 to 203)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                         GAAAACTCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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/clone lib="hog Library"
/note="Site l: BstXI; Libraries were prepared from
periphexal blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
10.9%; Score 44; DB 29; Length 203;
Best Local Similarity 55.1%; Pred. No. 3.4;
Matches 86; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 GCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                         CE091328,1 GI:35158174
                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (dog)
                                                                                        167 AGGAAAACGAGAA 179
                                                                                                                               46 AAAGAAAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-0200
Fax: 301-838-0208
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BX367419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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CE091328
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73; Conservative
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Fax: 301-838-0208
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         Sed primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 7
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CE329306
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Cother GSSs: RPCI-23-85AS.TV
Contact: Shaying Zhao
Cother GSSs: RPCI-23-85AS.TV
Contact: Shaying Zhao
Cother GSSs: RPCI-23-85AS.TV
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: schaodeigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (hito@aresgen.com). BAC end page:
http://www.tigr.org/tdb/bac
Plate: 85 row: A column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 bp DNA linear GSS 26-JUL-2000
RPCI-23-85A5.TJC RPCI-23 Mus musculus genomic clone RPCI-23-85A5,
genomic survey sequence.
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mogann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse, BAC End Sequences from Library RPCI-23
Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
httative full length read
vector to vector length is
Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pAMP1; The library was synthesized with modified SMART primers with dUTP at the end. After treatment with UDG the cDNA was cloned in pAMP1 vector by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:10090"
/tibsue_type="mnall intestinal epithelial progenitors"
/tibsue_type="mnall intestinal epithelial progenitors"
/clone_lib="BH5alpha Ultra Max cells (Invitrogen)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATGGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 14; Length 345;
Pred. No. 11;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                       /organism="Mus musculus"
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ilarity 52.9%;
Conservative 0
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Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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VERSION
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AZ273050
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/ask=Femmale"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lote="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AGAAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCCAAGAAAGGAAACCCCAGATGAGGAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 274)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ددرت 274 bp DNA linear GSS 26-SEP-20
tigr-gss-dog-17000333970436 Dog Library Canis familiaris genomic,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Mang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 41.8; DB 28; Length 160; 58.4%; Pred. No. 11; ive 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Canis familiaris"
|mol_type="genomic DNA"
|strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9615"
/clone_lib="Dog Library"
Location/Qualifiers
1. 160
/organism="Mus musculus"
                                                                                               /mol_type="genomic DNA'
/strain="C57BL/6J"
                                                                                                                                                     /db_xref="taxon:10090"
/clone="RPCI-23-85A5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CE329306
CE329306.1 GI:36144095
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Canis familiaris
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non-minichromosomal genome."
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Trypanosoma brucei
                                                                                                                                                                                                                         67; Conservative
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                                                                                                                                                                               Query Match
Best Local Similarity
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KEYWORDS
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AQ645726/c
                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 03-OCT-2000
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                                                                                                                                                                               AZ419893
1M0196A08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0196A08 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus 1 (bases 1 to 357)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                         /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                      Gaps
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                            99 GACTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAA 147
                                                                                       Length 274;
                                                                                                                                   Indels
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                                                                                     Query Match 10.3%; Score 41.8; DB 29;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 67; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0196 row: A column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 357.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:10090"
/clone="UUGC1M0196A08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ419893
AZ419893.1 GI:10543906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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AUTHORS
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AZ419893
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                                           ORIGIN
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/db_xref="taxon:569" |
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/clone="RPC193-EcoR1-4J12" |
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1. (Gastes I to 2.00.)

Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Donelson, J., Fraser, C. and Adams, M.

Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93

Library for gene discovery and sequence-ready map construction

Unpublished (1999)

Other GSSS: RPCI99-ECORI-4J12.TJ

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fex: 301 838 0200

Fex: 301 838 0208
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1999
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RPC193-ECORI-4J12.TV RPC193-ECORI Trypanosoma brucei genomic clone
RPC193-ECORI-4J12, genomic survey sequence.
AQ645726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nelsaye@tigr.org
Clones and high density filters may be purchased from BACPAC
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
gage: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 GACTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 41.2; DB 28;
60.9%; Pred. No. 17;
tive 0; Mismatches 43;
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/strain="TREU927/4 GUTat 10.1"
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AL725744 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA 2002 rerio cDNA CLORA CDNA CLORA BANAO78ZGOZ 5', mRNA sequence.
AL725744
BZT.25744.1 GI:20190348
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
153J05 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Ospriniformes; Osprinidae; Danio.

1 (Dases 1 to 244)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Aradelin,J.D., Weissenbach,J. and Petit,C.
A subtracted CDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 TATCTCCTGCGAAAACTCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAGAAAGGAAAC
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreféqenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                        139 AGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAA 179
                                                                                249 АААСААМАААААААААААТАААААААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%; Score 40.4; D
50.5%; Pred. No. 25;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BNOAA078ZG02"
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AL206710
AL206710.1 GI:7865529
GSS; genome survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Contact: Genoscope
Genoscope - Centra France
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5981.f For
more information about this cluster, see
http://www.genoscope.cns.fr
cgi-bin/cluster.cgi?seq-CSODF019DA09NPlkcluster=5981.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://tullength.invitrogen.com/ InvitroGen Corporation 1600
Faraddy Avenue Genoscope sequence ID: CSODF019DA09NPl.
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/clone_lib="Homo septens FETAL BRAIN"
/clone_lib="momo septens" bCWGBPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCWVSPORT 6
vector. Library was not normalized."
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                                                                                                                                                                    159 AAGCAGAGCTTGCAGAAAGAATGCAATGCAGCTGGAGACAACAAAACTGAATGTGGAA 100
                                                                                                                                                                                                               82 AGAAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 359)
                                                                                                                                                                                                                                                     99 AGAAACCTGGGTGCACTTACGACGCAACAAAAAGTGCACATTGAGTGAAGAACCA 40
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                                                                                                                               22 AAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCCAAAAAGGAAACCCCAGATGAGGAA
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                                          Length 276;
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                                                                                      Indels
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                                            DB 28;
                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 40.6; DE ilarity 49.1%; Pred. No. 23; Conservative 9; Mismatches
                                          10.0%; Score 40.6; DB
llarity 57.5%; Pred. No. 23;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODF019YB18"
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                                                                                                                                                                                                                                                                                               142 CAAGAAG 148
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Matches 79; Conserv
                                                                Local Similarity
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AU039357 ST 29-MAR-1999 ARNA linear EST 29-MAR-1999 AU039357 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLH629, MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         part of a large
nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (5-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at highest charten information, please take a look at Location/Qualifiers
AL178961.1 GI:7817018
GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Teleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracontoidea; Tetracodontidae; Tetracodon.
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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Genome Res. 10 (7), 939-949 (2000)
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/organism="Tetraodon nigroviridis"
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4; Mismatches
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Best Local Similarity 51.8
Matches 73; Conservative
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, stilnopterygii, Neopterygii, Taleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                       Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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llarity 36.1%; Pred. No. 28;
Conservative 25; Mismatches
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Matches 70; Conserv
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Dictyostelium.

1 (bases 1 to 372)

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Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takenoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostelium developmental CDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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Contact: Hideko Urushihara
Institute of Biological Sciences
Institute of Biological Sciences
University of Tuckuba, Ibaraki 305-8572, Japan
1-1.1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
1-1.298-53-4664
Fax: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostellum discoideum cDNA project in Japan'.
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9.8%; Score 39.6; DB 9; Length 37;
Best Local Similarity 54.9%; Pred. No. 40;
Matches 78; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostelium discoideum"
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/strain="AX4"
                                                                                                                                                                development
DNA Res. 5 (6), 335-340 (1998)
99156227
Dictyostelium discoideum
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Db 260 AGATAATAAGAAAAAGATAAT 281 Search completed: April 23, 2004, 02:33:55 Job time : 2027 secs

159 TTCTAATCAGGAAAACGAGAAT 180

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: April 22, 2004, 17:20:54; Search time 291 Seconds (without alignments) 5912.441 Million cell updates/sec	Title: US-10-005-907-1_COPY_25_429 Perfect score: 405 Sequence: 1 atgggaaattatctcctgcgatgaagttgtgtttccacac 405	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 3373863 segs, 2124099041 residues	Total number of hits satisfying chosen parameters: 4428564	Minimum DB seq length: 0 Maximum DB seq length: 405	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : N_Geneseq_29Jan04:* 1: geneseqn1980s:* 2: geneseqn1990s:* 3: geneseqn200ls:* 5: geneseqn200ls:* 6: geneseqn200ls:* 7: geneseqn200ls:* 8: geneseqn200ls:* 9: geneseqn2003as:* 10: geneseqn2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	Aaf24365 Retrovira	Abt22783 Breast ca	_	Human	Aai86998 Human pol	σ	Abs68189 cDNA enco	Adc25183 Human cDN	Abv54289 Human pro	Human	Abx39335 Bovine ES	Abl78974 Human ova		Abv58181 Human pro	Abv18573 Human pro	Abv50079 Human pro	Abx46789 Bovine ES	Abx47137 Bovine ES	Aai80160 Human pol	Abv57456 Human pro	Abv58773 Human pro	'n	Abv54241 Human pro
SUMMARIES	GI	AAF24365	ABT22783	AAZ12627	ABV18980	AA186998	AAS29049	ABS68189	ADC25183	ABV54289	AA185197	ABX39335	ABL78974	ABV54300	ABV58181	ABV18573	ABV50079	ABX46789	ABX47137	AA180160	ABV57456	ABV58773	ABV48535	ABV54241
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	% Query Match	9.6	9.5	9.5	9.2	0.6	9.0	0.6	9.0	9.9	6.8	8.9	6.8	6.8	8.8	8.8	8.7	8.7	8.7	8.7	8.6	8.6	8.6	8.6
	Score	38.8	38.6	37.2	37.2	36.6	36.4	36.4	36.4	36.2	36.2	36	36	36	35.8	35.6	35.4	35.4	35.4	35.2	35	35	34.8	34.8
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ALIGNMENTS

RESULT 1

AAF24365 standard; DNA; 172 BP. 24-APR-2001 (first entry) AAF24365;

Retroviral recombination assay coding sequence fragment #10.

Retroviral recombination assay; gene therapy vector; viral vector; gag; pol; replication; HIV; ds.

Unidentified.

WO200104360-A2

18-JAN-2001.

06-JUL-2000; 2000WO-US018597.

99US-0143015P. 99US-0164626P. 09-JUL-1999; 10-NOV-1999;

(UABR-) UAB RES FOUND. (TRAN-) TRANZYME INC.

Kappes JC, Wu X, Wakeield J;

WPI; 2001-091927/10.

Retroviral recombination assays, systems and cells, useful for evaluating the risk of producing a replication-competent retrovirus from a retroviral-based vector.

Example 5; Fig 14; 88pp; English.

The present invention describes a method for detecting a retroviral genetic recombinant having gag and pol functions, involving a cell suspected of having a recombinant and propagating the recombinant in the presence of any necessary helper functions. This is useful as it enables the detection of vectors which are able to replicate in the host cell, and allows the production of vectors suitable for gene therapy. The present sequence is a DNA fragment used to demonstrate the method of the invention

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selectively binds to a protein of a breast cancer marker gene is useful for treating cancers, particularly breast cancers. The host cell of the invention is useful for producing non-human transgenic animals. This polymucleotide sequence represents one of the breast cancer marker genes of the invention
                                                                    Sequence 403 BP; 145 A; 81 C; 68 G; 98 T; 0 U; 11 Other;
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                                                                                                                                      Cytostatic; vaccine; breast cancer marker gene; breast mass; immunogen; chemotherapy; tumour burden; bait protein; two-hybrid; three-hybrid; surrogate marker gene; pharmacodynamic marker gene; transgenic animal; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide encoded by breast cancer marker gene, useful for diagnosing, staging, monitoring, prognosing and treating diseases associated with breast cancer.
                                                Gaps
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                          5; Length 172;
                                                67; Indels
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   Sequence 172 BP; 148 A; 5 C; 10 G; 9 T; 0 U; 0 Other;
                        Score 38.8; DB
Pred. No. 0.29;
0; Mismatches
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                                                                                                                                                             TTCTAATCAGGAAACGAGAATGGCA 184
                                                                                                                                                                                  TTTTTAAAAGAAAGGGGGGGCTGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 247; 725pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2002; 2002WO-US012612.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC.
                          9.6%;
                                                                                                                                                                                                                                         ABT22783 standard; DNA; 403
                                                                                                                                                                                                                                                                                        (first entry)
                                    Local Similarity 54.1
ses 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                       16-APR-2003
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                                                                                                                                                                                                                                                                 ABT22783;
                         Query Match
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                                                                                                                 81 AAGAAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAG 140
                                                                                                                                              Novel human genes and their expression products which are differentially expressed in different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escobedo J, Innie MA, Garcia PD, Sudduth-Klinger J;
Jiese K, Randazzo F, Kennedy GC, Pot D, Kasaam A;
nanac R, Cikvenjakov R, Dickson M, Drmanac S, Labat I;
Kita D, Garcia V, Jones WL, Stache-Crain B;
                                                                                     21 AAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGATGAGGA
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Human, gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                               ;
0
9.5%; Score 38.6; DB 7; Length 403; 53.6%; Pred. No. 0.44; tive 0; Mismatches 64; Indels (
                                                                                                                                                                                                                                                                                                                                                                     Human gene expression product cDNA sequence SEQ ID NO:96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 684; 2479pp; English.
                                                                                                                                                                                                                                                                                 AAZ12627 standard; cDNA; 283 BP.
                                                                                                                                                                             141 CCAAGAAGTTTCATCCAC 158
                                                                                                                                                                                                         329 CAPATATCCCTTAAACAC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0075954F.
98US-0080114P.
98US-0080515P.
98US-0105234P.
98US-0105234P.
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                 Local Similarity 53.6
nes 74; Conservative
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Drmanac R,
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Reinhard C, G
Lamson G, Drm
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21-OCT-1998;
28-OCT-1998;
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31-MAR-1998;
03-APR-1998;
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                                Matches
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The invention relates to an isolated polypeptide encoded by a breast cancer marker gene comprising any of 1417 21-805 nucleotide sequences, given in the specification. The methods of the invention are useful for diagnosing patients having an identified breast mass or symptoms associated with breast cancer, to diagnose breast cancer or its precursors, and for monitoring the efficacy of treatment of a breast cancer patient (e.g. efficacy of chemotherapy). The methods are also useful for evaluating a patient before, after or during therapy, to evaluate the reduction in a two-outen. The breast cancer marker gene proteins are useful as immunogens for raising antibodies, by immunising a mammal with a breast cancer marker proteins are useful as bait proteins in two-hybrid or three-hybrid assay, to identify other proteins in two-hybrid or interact with the marker proteins. The breast cancer marker genes are useful as surrogate marker proteins. The breast cancer marker genes are useful as surrogate marker genes for one or more disorders, disease states or conditions leading to disease states, in particular, breast cancer marker genes. An antibody which

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differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product in a cest sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 548 polymucleotide sequences given in AA21253 to AA217779. The polymucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymuchophisms. Polypeptides encoded by the polymucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polymucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an exceptible of a genetic predisposition or susceptibility to a disease such as cancer). The polymucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polymucleotides can also be used to screen for peptide analogues and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAATCAAAAGAAGCCCAAGAAAGGAAACCCCAGATGAGGAAAGGAAAACGGCAGGAAATGA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 CTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of
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0
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                                                                                                                                                                                                                                                                                                                                                                                                   88; Indels
                                                                                                                                                                                                                                                                                                                                Sequence 283 BP; 20 A; 27 C; 34 G; 126 T; 0 U; 76 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 CTAATCAGGAAACGAGAATGGCAGTGGTTCTGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAANNCAAGNTANAAANNATGNTAACNANNGTGA 102
                                                                                                                                                                                                                                                                                                                                                               Query Match 9.2%; Score 37.2; DB Best Local Similarity 42.9%; Pred. No. 1; Matches 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 18971.
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit ing prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                     8 ATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGGCCCAAGAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                               9.2%; Score 37.2; DB 5; Length 384; 50.6%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                    76; Indels
                                                                                                                                                                                                                                                                                                               Sequence 384 BP; 163 A; 57 C; 23 G; 82 T; 0 U; 59 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AAGATAAGAAAAGCCAAGAAGTTTCATCCACTTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AANANAAAAAAAAAAAAAAAAAAATTCNNNNC 154
                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1;
0; Mismatches
                                                   Claim 1; Page 3116; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 7058.
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18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.6
nes 78; Conservative
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P-PSDB; AAO07067.
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14-ANG-2000)
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14-ANG-2000)
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
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25-SEP-2000;
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Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation; gene transcription; malignant disease; autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease; neurological disorder; gene therapy; immunomodulatory; anti-HIV; anti rheumatic; anti microbial; cytostatic; ss.
                                                                                                                                                                                                                                                                               99 GACTACATTIGAAAGAAAACTICAAGAICAAGAIAAGAAAAGCCAAGAAGITTCATCCAC 158
                               t
C
                                                                                                                                                                                                                                                          The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to yrtokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or resament of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                           DB 4; Length 390;
Claim 1; SEQ ID NO 7058; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                               64; Indels
                                                                                                                                                                    Sequence 390 BP; 229 A; 48 C; 49 G; 57 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding for human DNA-binding protein #20.
                                                                                                                                                                                                     Best Local Similarity 54.0%; pred. No. 1.7; Matches 0; Mismatches
                                                                                                                                                                                            9.0%; Score 36.6;
                                                                                                                                                                                                                                                                                                                          159 TICTAATCAGGAAAACGAG 177
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2000US-0189874P.
2000US-0190076P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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16-MAR-2000;
17-MAR-2000;
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The present invention relates to the isolation of novel DNA-binding proteins (AAU18154-AAU18281), and cDNA and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, droromo (chromatin organisation modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonism and/or agoing assays to identify antagonism and/or agoinsts that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 30; 561pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                 2000US - 0246475P

2000US - 0246476P

2000US - 0246478P

2000US - 0246523P

2000US - 0246525P

2000US - 0246527P

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2000US-0251989P.
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P-PSDB; AAU18173.
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08-NOV-2000;
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05-JAN-2001;
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diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's disease). The polymucleotide sequences of the invention may also be used in gene therapy. AAS29030-AAS29157 represent sequences encoding for novel DNA-binding proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                              Human, DNA-binding protein, B cell immunodeficiency, autoimmune disorder, severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease, diabetes mellitus, allergy; asthms; inflammatory condition; thrombosis; graft-versus-host disease; blood-related disorder; atherosclerosis; hyperproliferative disorder; cancer; renal disorder; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperproliferative disorder; renal disorder; arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory disorder; golomerulonephritis; cardiovascular disorder; respiratory disorder; goodpasture's syndrome; neurological disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; gene; reproductive system disorder; endometrisals; infections disease; viral infection; bacterial infection; fungal infection; vaccine; gastrointestinal disorder; multiple sclerosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                            6 AAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAAGAAGCCCAAGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                           66 AAACCCAGATGAGGAAAGAAAACGGCAGGAAATGACTACATTTGAAAAGAAAACTTCAAGA
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                                                                                                                                                                                                                                         Query Match
9.0%; Score 36.4; DB 5; Length 325;
Best Local Similarity 53.5%; Pred. No. 1.8;
Matches 76; Conservative 0; Mismatches 66; Indels (
                                                                                                                                                                                                         Sequence 325 BP; 174 A; 38 C; 36 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding human DNA-binding protein #20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 TCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 AAAAAAAAAAAAAAAAA 323
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04-FEB-2000; 2000US-018062BP.
28-UJN-2000; 2000US-021468FP.
07-JUL-2000; 2000US-0216647P.
11-JUL-2000; 2000US-021689P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-021896P.
26-JUL-2000; 2000US-021896P.
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2000US-02108290P.
2000US-0220964P.
2000US-0224518P.
2000US-0224519P.
2000US-0225267P.
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2000US-0228924P.
2000US-022934P.
2000US-0229343P.
2000US-0229344P.
2000US-0229345P.
2000US-0229345P.
2000US-0229509P.
2000US-0229509P.
2000US-0239513P.
2000US-023423P.
2000US-023423P.
                                                            2000US-0236368P.
2000US-0236369P.
                                                                                                            08-DEC-2000; 2000US-0251868P
08-DEC-2000; 2000US-0251869P
                                                                                             20-OCT-2000;
                                                                                                   01-NOV-2000
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(ROSE/) ROSEN C A. (RUBE/) RUBEN S M. (BARA/) BARASH S C.

Barash SC; Rosen CA, Ruben SM,

WPI; 2002-690611/74. P-PSDB; ABG92594.

Novel DNA-binding protein useful for diagnosis, prognosis, prevention and treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.

Claim 1; SEQ ID NO 30; 225pp; English.

The present invention relates to a new DNA-binding protein. The invention is useful in treating, preventing, diagnosing and/or prognosing immunodeficiencies (severe combined immunodeficiencies), autoimmune disorders (theumatoid arthritis, multiple sclerosis, diabetes mellitus), allergic reactions and conditions (e.g. cathma), inflammatory conditions, graft-versus-host disease, blood-related disorders (thromosis, atherosclerosis), hyperproliferative disorders (e.g. cancer), renal disorders (e.g. acute glomerulomephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's disease), reproductive system disorders (e.g. endometricsis), infectious disease), reproductive system disorders (e.g. endometricsis), infectious disease), reproductive system disorders (e.g. endometricsis), infectious disease), reproductive system disorders (e.g. endometricsis), infectious disease), reproductive system disorders (e.g. cohn's disease). The invention is also cuseful to stimulate neuronal growth and treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-capes minding protein of the invention. Note: The sequence encodes a human DNA-binding protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was cobtained in electronic format directly from USPTO at

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6 AAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCCAAGAAAGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular matrix protein, cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiants-cardiavoscular-Gen; nephrotropic; antihilammancory; muscular-Gen; respiratory-Gen; immunosuppressive; cerebroprotective; vesotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder; miscular disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; renal disorder; inflammatory disorder; proliferative disorder; human; gene therapy; ss; inflammatory disorder; proliferative disorder; human; gene therapy; ss;
                                                            Gaps
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0
                             DB 6; Length 325;
                                                            66; Indels
Sequence 325 BP; 174 A; 38 C; 36 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA from extracellular matrix gene 20.
                             Score 36.4; DE
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                              126 TCAAGATAAGAAAGCCAAGAA 147
                                                                                                                                                                                                                                           302 AAAAAAAAAAAAAAAAAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000; 2000US-0179065P.
24-FEB-2000; 2000US-01864664P.
22-MAR-2000; 2000US-01864664P.
02-MAR-2000; 2000US-0186350P.
15-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0199123P.
07-JUN-2000; 2000US-0205515P.
07-JUN-2000; 2000US-0214886P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
                             Query Match
Best Local Similarity 53.5%;
Matches 76; Conservative C
                                                                                                                                                                                                                                                                                                                        ADC25183 standard; cDNA; 325
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New DNA-binding proteins and gene encoding them, useful for diagnosing, treating and/or preventing e.g. neurological, inflammatory, infectious, cardiovascular, autoimmune, respiratory, neoplastic or digestive
                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                               HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                           Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                      WPI; 2003-605749/57.
P-PSDB; ADC25311.
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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                                                                                                                          17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                               05-DEC-200
                                                                                                                                                                                                                                                                                                         diseases.
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The invention relates to an isolated nucleic acid molecule (CDNA)

c accoding a human extracellular matrix protein, representing one of 161

c novel genes. Also included are recombinant vectors, host cells

c novel genes. Also included are recombinant vectors, host cells

c novel specially, the extracellular matrix proteins (including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition in the nucleic acid and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or control or amount of expression of the protein in a biological sample and diagnosing a condition based on the protein to a mamunian subject, identifying a binding partner to the protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the cDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the supernatant, detecting an activity in a biological Claim 1; SEQ ID NO 30; 226pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                          6 AAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGG
                                                                                            Gaps
assay and identifying the protein in the supernatant having the activity). The nucleic acids and proteins display the following activities Cytostatic, antibacterial, Virucide, Neuroprotective,
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                                                            Length 325;
                                                                                            66; Indels
                                                              DB 9;
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate expression marker cDNA 54280
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                                                            Score 36.4;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 10498; 11750pp; English
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                                                                                                                                                                                                                                                     126 TCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                                                                                                                                   ABV54289 standard; cDNA; 346 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
; 2000US-025281P.
                                                            9.08;
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                                             Ouery Match
Best Local Similarity 53...
Best Local 6, Conservative
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18-JUL-2000;
13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                ABV54289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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133
                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptidd therapy, stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                     14 TCCTGCGAAAACTCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAG 73
                                                                                                                                                       Gaps
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                                                 Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 5257; 1399pp + Sequence Listing; English.
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 396 BP; 178 A; 47 C; 100 G; 71 T; 0 U; 0 Other;
                 Sequence 346 BP; 138 A; 85 C; 52.G; 71 T; 0 U; 0 Other;
                                                                                       68;
                                                    DB 5,
                                                                     2.1;
                                                                                   0; Mismatches
                                                 Score 36.2;
Pred. No. 2.
                                                                                                                                                                                                                                                                 134 AGAAAAGCCAAGAAGTTTCATCCAC 158
                                                                                                                                                                                                                                                                                                   134 AAAAAAAAAAAAAAGGGGCCCCCCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO 5257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rang YT, Liu C, Drmanac RT;
                                                   Query Match
Best Local Similarity 53.1%;
Matches 77; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                          AA185197 standard; cDNA; 396
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001.
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The Invention relates to a pullitue increase and increation or muscle and fat deposition (designated IMPD), derived from cattle, and the IMPD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1812 nucleotide sequences, appearing as ABX48836-ABX49847, or complements of them. Also included are it. It atransformed cell having a nucleic acid comprising an IMPD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell having a nucleic acid comprising an IMPD nucleic of polyadenylated ribonucleotides to a 3 end of the MRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising. (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridiaation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                     80 AAAGAAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAA 139
                                                                                                                                                                           20 GAAAACTCCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGATGAGG 79
                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                   Gaps
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                                                    ;
                4; Length 396;
                                                    Indels
                                                  53;
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              Score 36.2; DB Pred. No. 2.2; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                            ABX39335 standard; cDNA; 343 BP
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                  8.9%;
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Query Match
Best Local Similarity 56.2
Local 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
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(WARR/) WARREN W C.
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and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynuclectide (III) having a cDNA sequence (S1) from the 10912 nuclectide sequences as given in ABL77023 to ABB47934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonuclectide (IV) that hybridises to (S1) can be used for
detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMF EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                              130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention describes a composition (I) comprising: carriers
                                                                                                                                                                                                                                                                                                                                                                                96 AATGACTTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian timor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
                                                                                                                                                                                                                                              DB 7; Length 343;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                           Sequence 343 BP; 169 A; 56 C; 57 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian cancer related cDNA clone SEQ ID NO:1952.
                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                            Score 36; DB Pred. No. 2.4; 0; Mismatches
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                                                                                                                                                                                                                                                          Similarity 55.6%;
69; Conservative
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                                                                                                                                                                                                                                                              Local Similarity
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progression of prostate cancer in a patient; (c) assessing the efficacy

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serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polymuclectide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polymuclectide hybridising to (IV) is detected preferably by polymerses chain reaction (PCR). (I) comprising (III) and/or [II] is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells specific for an ovarian tuseful in design and preparation of ribosyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques
   detecting ovarian cancer in a patient's biological sample preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 381 BP; 102 A; 58 C; 60 G; 157 T; 0 U; 4 Other;
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ö 95 AAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAAGCCAAGAAGTTTCAT 154 156 AATTAAACTCAGTGGAAAATAATTTTCAAGAAAAAGAAGAAAATAGACAAGCTGACTAAA 97 Gaps 8.9%; Score 36; DB 6; Length 381; 2.0%; Pred. No. 2.5; ve 0; Mismatches 35; Indels CCACTTCTAATCAGGAAACGAGAATGGCAGT 186 65 CAAATTATGATTATGAAATAAGGTAGGCAGT 62.0%; Local Similarity 62.0 les 57; Conservative 155 96 Query Match Matches 쉽 ઠ ጵ g

ABV54300 standard; cDNA; 382

ABV54300

(first entry) 17-SEP-2002 Human prostate expression marker cDNA 54291

Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

Homo sapiens

WO200160860-A2

23-AUG-2001

20-FEB-2001; 2001WO-US005171

2000US-0183319P. 17-FEB-2000; 25-MAY-2000; 16-MAR-2

2000US-0207454P. 2000US-0211314P. 2000US-0219007P. 2000US-0255281P 13-DEC-2000; PREDICTIVE MEDICINE INC. (MILL-) MILLENNIUM

Monahan JE;

WPI; 2001-662795/76

Schlegel R, Endege WO,

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

Claim 1; Page 10500; 11750pp; English

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV6010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the ABSULT 13
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           of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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pharmacogenomic marker, gene; ss.
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                                                                                                                                                                       Length 382;
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                                                                                                                                         Sequence 382 BP; 179 A; 68 C; 62 G; 73 T; 0 U; 0 Other;
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0; Mismatches
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                                                                                                                                                                         Score 36;
Pred. No.
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-0211314P.
13-DEC-2000; 2000US-0219007P.
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Best Local Similarity 54.5:
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of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has mecastabized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                           TCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAG
                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                        Query Match 8.8%; Score 35.8; DB 5; Length.317; Best Local Similarity 51.2%; Pred. No. 2.6; Matches 82; Conservative 0; Mismatches 78; Indels C
                                                                                                                                         Sequence 317 BP; 146 A; 44 C; 30 G; 96 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                 134 AGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAA 173
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18-JUL-2000;
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16-MAR-2000;
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the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (1) is also useful as a pharmacodyanamic or pharmacogenomic marker
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/ (gnz 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
/ (gnz 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2907579 segs, 2254313464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications NA:* . /cqn2 6/btodata/1/pubpna.
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                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1156, Ap	Sequence 101964,	Sequence 95566, A	Sequence 30, Appl	Sequence 30, Appl	Sequence 41873, A	Sequence 4500, Ap	Sequence 1952, Ap	Sequence 418, App	Sequence 98076, A	Sequence 94516, A	Seguence 11954, A	Sequence 12302, A	Sequence 55157, A
ΩΙ	US-10-125-968-1156	US-10-424-599-101964	US-10-424-599-95566	US-09-764-846-30	US-10-091-483-30	US-10-424-599-41873	US-09-960-352-4500	US-09-867-701-1952	US-09-969-373-418	US-10-424-599-98076	US-10-424-599-94516	US-09-960-352-11954	US-09-960-352-12302	US-10-424-599-55157
DB	16	13	13	σ	15	13	σ	6	σ	13	13	σ	σ	13
% Query Match Length DB	403	347	345	325	325	379	343	381	193	282	340	332	341	368
% Query Match	9.5	9.5	9.5	0.6	0.6	в. Ф.	8.9	8.9	8.8	8.8	8.8	8.7	8.7	8.7
Score	38.6	38.4	37.4	36.4	36.4	36.2	36	36	35.6	35.6	35.6	35.4	35.4	35.2
Result No.	ı	2	m	4	'n	y	7	ω	σı	10	11	c 15	c 13	14

89471,	Sequence 21648, A	39861,	49770,	49770,	Seguence 139195,		52791	equence 1621,	97494	equence 4	11030	48934	13382	4	Sequence 10761, A	Sequence 3292, Ap	Seguence 7042, Ap	Seguence 15028, A			Sequence 131162,	83670	10	õ	Sequence 567, App	ŵ	52	e 22	488	Sequence 25361, A
US-10-424-599-89471	-424-599-2	0-424-599-	3-085-78	0-242-	0-424-599-13919	0-424-	US-10-424-599-52791	0-102-	0-424	US-09-814-353-4733	-814-353-1	US-10-424-599-48934)-282-122A-133	US-10-424-599-85844	US-09-867-701-10761	US-09-960-352-3292	US-09-960-352-7042	US-10-085-783A-15028	535A-1	US-09-814-353-17367	US-10-424-599-131162	US-10-424-599-83670	9-237-183A-10	US-09-960-352-4808	-925-299	σ	-085-78	1-242-53	US-09-960-352-4884	US-10-424-599-25361
13	13	13	13	16	13	13	13	15	13	10	10	13	13	13	φ	σ	σ	13	16	10	13	13	10	σ	0	ដ	13	16	σ	13
327	342	348	234	234	270	306	309	183	344	358	358	391	195	283	290	299	309	319	319	362	388	279	318	392	208	208	235	235	332	341
9.8	9.8	9.8	9.8	9.8	8.6	8.6	8.6	8.5	8.5	80	8.5	8.5	8.5	8.5	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.3	8.3	8.3	8.3	8.3	8.3
35	35	35						34.6	34.6	34.6	34.6	34.6	34.4	34.4	34.2	34.2	34.2	34.2	34.2	34.2	34.2	m			m	ω,		ന	m	 س
15	16	11	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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GENERAL INTOCANTIANT INTOCANTIANT INTOCANTIANT INTOCANTIANT INTOCANTIANT INTOCANTIANT INTOCANTIANT INTOCANTIANT INTOCANTIANT Palermo, Adam

APPLICANT: Wang, Youthen

APPLICANT: Staimman, Kathleen

APPLICANT: Elias, Josh

APPLICANT: Elias, Josh

APPLICANT: Mertens, Maureen

APPLICANT: Mertens, Maureen

APPLICANT: Mertens, Maureen

APPLICANT: Mertens, Maureen

APPLICANT: Mertens, Maureen

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE OF INVENTION: THERAPY OF BREAST CANCER

FILE REPERENCE: MRI-032

CURRENT APPLICATION NUMBER: US/10/125,968

CURRENT APPLICATION NUMBER: US 60/285,163

FRIOR APPLICATION NUMBER: US 60/285,163

FRIOR FILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 1417

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1156

LENGTH: 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Homo sapiens

) FEATURE:

NAME/KEY: misc feature

) LOCATION: 30, 57, 85, 100, 118, 154, 219, 224, 226, 247, 261

) OTHER INFORMATION: n = A,T,C or G
Sequence 1156, Application US/10125968 Publication No. US20030215805A1 GENERAL INFORMATION:
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Gaps

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99 GACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCAC 158
                                                                                                                                                                                                                                       6 AAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAGAATCAAAAGAAGCCCAAGAAAGG
            Query Match
9.2%; Score 37.4; DB 13; Length 345;
Best Local Similarity 55.9%; Pred. No. 1.3;
Matches 71; Conservative 0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PIZZOL
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICANION WUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
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Pred. No. 2.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 TCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AAAAAAAAAAAAAAAAAAAAAAA 323
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Best Local Similarity 53.5%;
Matches 76; Conservative
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CRGANISM: Homo sapiens
US-10-091-483-30
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US-09-764-846-30
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/28684
SEQ ID NOS: 285684
LENGTH: 345
                                                                                                                                                                                                                                                                        Sequence 101964, Application US/10424599
Sequence 101964, Application US/10424599
Sequence 101964, Application US/20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acvalic David K
APPLICANT: Acvalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 288684
SEQ ID NO 101964
LENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AAGAAAACGGCAGGAAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAG 140
                                                                                      269 TCATAATCAAAAAGGCAGCCCTAAGAATAAATGAAAAGTTCACAGAAAAAAATAAAAATG 328
101 CTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38.4; DB 13; Length 347; Pred. No. 0.69; 0; Mismatches 76; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 CTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAAGT 200
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US-10-424-599-95566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: PAT_MRT3847_6308C.1
US-10-424-599-101964
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                                                                                                                                    CCAAGAAGTTTCATCCAC 158
                                                                                                                                                                             329 caaararcccrraaacac 346
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Best Local Similarity 52.5%;
Matches 84; Conservative 0
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95 AAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCAT 154
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; Sequence 1952, Application US/09867701
; Patent No. USC020132237A1
; GENERAL INFORMATION:
APPLICANT: AJate, Paul A.
APPLICANT: AJate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COVARIAN CANCER
FILE REFERENCE: 21011.497
; CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
; SEQ ID NO 1952
; SEQ ID NO 1952
; LENGTH: 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 381;
                                                                                                                                Length 343;
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APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10[52679]A
CURRENT APPLICATION NUMBER: US/99/969,373
CURRENT FILING DATE: 2001-10-02
                                                                                                                                                                         55; Indels
                               ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-BOVMS1-017-Q1-E1-E11
US-09-960-352-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

8.9%; Score 36; DB 9;

Best Local Similarity 62.0%; Pred. No. 3.6;

Matches 57; Conservative 0; Mismatches 3
                                                                                                                           Query Match

8.9%; Score 36; DB 9;
Best Local Similarity 55.6%; Pred. No. 3.4;
Matches 69; Conservative 0; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 CCACTICTAATCAGGAAAACGAGAATGGCAGT 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 418, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                          156 CACT 159
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US-09-867-701-1952/c
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LENGTH: 343
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APPLICANT: Warren, Wesley C.
APPLICANT: Byat., John C.
APPLICANT: Byat., John C.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298) C.
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ ID NO 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: En Rosa Thina
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 41873
LENGTH: 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AAATTATCTCCTGCGAAAACTCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAGAAAGG 65
                                                Gaps
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  Length 325;
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    9.0%; Score 36.4; DB 15; Length ilarity 53.5%; Pred No.2.5; Conservative 0; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

8.9%; Score 36.2; DB 13;

Best Local Similarity 53.1%; Pred. No. 3.1;

Matches 77; Conservative 0; Mismatches 68;
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US-10-424-599-41873
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41873, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              126 TCAAGATAAGAAAAGCCAAGAA 147
                                                                                                                                                                                                                                                                                                                       302 AAAAAAAAAAAAAAAAAAAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Glycine max
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-960-352-4500
    Query Match
Best Local Simi:
Matches 76;
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Sequence 11947.4 Application US/09960352

Sequence 11954.4 Application US/09960352

Betent No. US2002013113941

GENERAL INFORMATION:

APPLICANT: Warren, Weisley C.

APPLICANT: Tao, Nengbing

APPLICANT: Mathialagan, Nagapan

APPLICANT: Mathialagan, Nagapan

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFRENCE: 1651.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11954

LENGTH: 332
                   and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 CTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTT 160
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (33223) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 94516 LENGTH: 340
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                                                                                                                                                                                                                                                                                                     DB 13; Length 340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 CACATTAATAAAATAAAAGGCGGCGGATTTTAAAAAGTTT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFPRATION: Clone ID: 51-LIB3058-058-Q1-K1-E4
US-09-960-352-11954
                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT3847_56359C.1
US-10-424-599-94516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                   Score 35.6; DB; Pred. No. 4.4; O; Mismatches
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Pred. No. 5;
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.2%;
Matches 83; Conservative
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                                                                                                                                                                                 TYPE: DNA
ORGANISM: Glycine max
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US-09-960-352-12302/c
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Publication No. US20040031072A1
CENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Avalic David K
APPLICANT: Avalythus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEC ID NOS: 285684
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                                                                                                                                                                                                                                                  Score 35.6; DB 9; Length 193;
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Pred. No. 4.1;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59576C.1
US-10-424-599-98076
                                                                                                                                                                                                                                                                                        0; Mismatches
  PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
LENGTH: 193
                                                                                                                                                                                                                                                                       Pred. No.
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                                                                                                                                                                                                                                                  8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.6%;
Matches 71; Conservative
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.0
Matches 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                  type: DNA Clycine max US-09-969-373-418
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US-10-424-599-94516
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Can Usina
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 89471
LENGTH: 327
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18 GCGAAAACTCAGTTGCCTGGGAGAATCAAAAGAAGCCCAAGAAAGGAAACCCAGATGA
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Pred. No. 6.5;
0; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 ddaaacaaacaaccecaaaaaacaacaccecaaccaaa 308
                                                                          159 ITCTAATCAGGAAAACGAGAATGGCAGTGGTTCTGAAGAA 198
                                                                                                                        129 riradagaarcadagrrracriccccciccriccadagaa 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COTHER INFORMATION: unsure at all n locations FEATURE: OTHER INFORMATION: clone ID: PAT_MRT3847_51802C.1 US-10-424-599-89471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 23, 2004, 04:03:59
Job time : 298 secs
                                                                                                                                                                                                                                           Sequence 89471, Application US/10424599
Publication No. US20040031072A1
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Best Local Similarity 59.0%;
Matches 59; Conservative
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ORGANISM: Glycine max
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APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323.)8
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
ENGIH: 368
LENGTH: 368
                                                               APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLERC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12302
LENGTH: 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 GACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAAGCCAAGAAGTTTCATCCAC 158
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8.7%; Score 35.4; DB 9; Length 341;
Best Local Similarity 53.2%; Pred. No. 5.1;
Matches 75; Conservative 0; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 53-BOVMS1-009-Q1-E1-F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 78;
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OTHER INFORMATION: unsure at all n locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.2;
Pred. No. 6;
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Publication No. US20040031072A1
GENERAL INFORMATION:
       Sequence 12302, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 TICTAATCAGGAAAACGAGAA 179
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Best Local Similarity 51.2%;
Matches 82; Conservative
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ALI GNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-09-621-976-8976
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YY 283
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Sequence 1322, Ap
Sequence 1324, Ap
Sequence 4053, Ap
Sequence 3835, Ap
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4555, Ap
25, Appl
25, Appl
32, Appl
32, Appl
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7, Appli
7, Appli
7, Appli
7, Appli
                                                                             April 22, 2004, 18:37:20 ; Search time 64 Seconds (without alignments) 3511.799 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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Sequence 2
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5.1.6
Compugen Ltd
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US-09-621-976-1322
US-09-621-976-1324
US-08-956-171E-4053
US-08-956-171E-4053
US-08-956-171E-4053
US-08-956-171E-4053
US-08-628-417-6
US-08-628-417-6
US-08-897-126-29
US-08-897-126-29
US-08-956-171E-4397
US-09-9713-550-16
US-08-97-13-550-16
US-08-97-13-550-16
US-08-97-126-22
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US-08-97-126-22
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US-08-97-126-22
US-08-97-126-22
US-08-956-171E-4555
US-08-956-171E-4555
US-08-956-171E-4555
US-08-956-171E-4555
US-08-956-171E-4555
US-08-956-171E-4555
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US-08-956-171E-4555
US-08-956-171E-4555
US-08-956-171E-4555
US-08-957-126-25
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                682709 seqs, 277475446 residues
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GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    nucleic search, using sw model
                                                                                                                                    US-10-005-907-1_COPY_25_429
                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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             Copyright
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Maximum DB seq length: 405
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Match 1
                                                                                                                                     Title:
Perfect score:
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                                                     OM nucleic
                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                   Searched:
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123 AGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGAATGG 182
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10254, A
16692, A
4, Appli
4, Appli
4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 CAGTGGTTCTGAAGAAGTGTGCTACACTGTCATTAATCACATCCCCCATCAGAGATCCTC
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                                                                                                                                                                                       Sequence 4, A Sequence 30, Sequence 30,
                                                                      Sequence 20,
Sequence 1289
Sequence 1025
                    Sequence 4, Sequence 4, Sequence 4,
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Sequence 4,
Sequence 4,
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8.6%; Score 34.8; DB 4; Length 399;
Best Local Similarity 12.4%; Pred. No. 0.26;
Matches 30; Conservative 110; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8976, Application US/09621976
Fatent No. 6639063
Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT FPLICATION NUMBER: US/09/621,976
CURRENT PRING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NOS: 19335
SEQ ID NO 8976
US-08-557-3098-4
US-08-857-3098-4
US-08-893-674A-4
US-09-297-555-20
US-09-621-976-10294
US-09-621-976-10294
US-09-621-976-10294
US-09-621-976-10692
US-09-61-976-10692
US-08-31A-4
US-08-31A-4
US-08-520-678-30
US-08-520-678-30
US-08-520-678-30
US-08-520-678-30
US-08-520-678-30
US-08-521-976-106-30
US-08-521-976-106-30
US-08-621-976-106-30
US-08-621-976-106-30
US-08-621-976-106-30
US-08-621-976-106-30
US-08-621-976-106-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 240;
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                                                                                                                                                                                                                                                                                                                                                       49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1324
LENGTH: 240
                                APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: EGTS and Encoded Human Proteins.
FILE REFERENCE: GENEET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1322
LENGTH: 249
                                                                                                                                                                                                                                                                                                                    Score 33.6; DB
Pred. No. 0.49;
0; Mismatches
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US-08-956-171E-4053
; Sequence 4053, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1324, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
Dumas Milne Edwards, J.B
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.2%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.07
Best Local Similarity 57.07
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAME/KEY: CDS
; LOCATION: 28..240
US-09-621-976-1324
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; NAME/KEY: CDS
; LOCATION: 28..249
US-09-621-976-1322
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Steven T. Farmon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
Steven C. Barash
Michael R. Farnon
MINDER Steven S. Standon
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 TTCAAGATCAAGATAAGAAAAGCCAAAGAAGTTTCATCCACTTCTAATCAGGAAAACGAGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 Grcagcaacaagergaarracaraaaaarraagercgarrgcgaargarraagaggga 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 acaaaggararracriargcaaaggaggaarcacargrigrigaracrigaaaaacaac 86
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8.1%; Score 33; DB 4; Length 400;
Best Local Similarity 54.5%; Pred. No. 0.93;
Matches 66; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 3, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTONEY, AGENT INFORMATION:
NAME: MARK J. Hyman
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4053:
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Patent No. 659314
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                          STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 309-84
INFORMATION FOR SEQ ID NO: 4053
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38 GAGAGAATCAAAAAGAAGCCCAAGAAAGGAAACCCAGATGAGGAAAAGAAAACGGCAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08628417

Patent No. 5627054

GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: DFFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEN PROVING GROUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
            MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MD COMPUTER: IBM compatible PC OPERATING SYSTEM: Windows 95 SOFTWARE: Word 97 (DOS text format) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/018,584A FILING DATE: 04-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.8%; Score 31.6; Di
Best Local Similarity 56.9%; Pred. No. 2.3;
Matches 58; Conservative 0; Mismatches
                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTATION UNDER: 29,018
REFERENCE/DOCKET UNDER: 16026
TELECOMMUNICATION INFORMATION:
TELEFAX: (608) 257-2501
TELEFAX: (608) 257-2255
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 bp
TYPE: Nucleic Acid
STRANDENESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pGem3Zf(+)
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ATTORNEY AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 15q26.2
US-09-018-584A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Circular MOLECULE TYPE: Genomic DNA HYPOTHETICAL: no IMMEDIATE SOURCE:
COMPUTER READABLE FORM
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G539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-628-417-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 CTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAAGCCAAGAAGTTTCATCCACTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 crattacricaaaaacaaccaccaacaacaaccicaartacataaaaaaatrargciccarric 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09018584A
Sequence 27, Application US/09018584A
Patent No. 623863
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schumm, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: REPEAT DNA MARKERS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSE: Promeça Corporation
STREET: 2800 Woods Hollow Road
                                                                                                                             COUNTRY: USA

ZIP: 20850

ZIP: 20850

COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE ASCII Taxt
CURRENT APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: CURROWN->
PRIOR APPLICATION NUMBER: 06/09,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORIEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEFRORE: (240) 314-1224
TELEFRORE: (240) 314-1224
TELEFRORE: (301) 309-8439
INFORMATION FOR SEG ID NO: 3835:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.9%; Score 31.8; DB 4; Length 400; Best Local Similarity 51.8%; Pred. No. 2.2; Matches 72; Conservative 0; Mismatches 67; Indels
                        CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 3835:
US-08-956-171E-3835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 CGAATGATTTAAGAGGAA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 CTAATCAGGAAAACGAGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
    NUMBER OF SECUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Wisconsin
PRY: U.S.A.
53711-5399
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US-09-018-584A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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DB 3; Length 372;

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Query Match
7.7%; Score 31; DB 3
Best Local Similarity 56.3%; Pred. No. 3.7;
Matches 58; Conservative 0; Mismatches
                                                              pGem3Zf(+)
                                                                                                                                                                   4 gter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base paire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                               POSITION IN GENOME:

; CHROMOSOME/SEGMENT:

US-09-018-584A-13
                                      : plasmid,
G132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 65; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
HYPOTHETICAL: no
IMMEDIATE SOURCE:
LIBRARY: plasmi
CLONE: G132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-520-678A-29
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STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Schumm, James W.
APPLICANT: Schumm, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Jeffer, Je
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 7.7%; Score 31; DB 1; Length 240; Similarity 52.8%; Pred. No. 3.1; 67; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
FILING DATE: 04-Feb-1998
CLASSIFICATION:
ATTORNEY/ACEPTED
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: oligodeoxynucleotide
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-018-584A-13/c; Sequence 13, Application US/09018584A; Patent No. 6238863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Promega Corporation
2800 Woods Hollow Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTARION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026
TELECOMMUNICATION INFORMATION:
TELEFONE: (608) 257-251
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                               TELECOMMUNICATION INFORMATION TELEPHONE: 410-671-1158 TELEFAX: 410-671-2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic DNA
      REFERENCE/DOCKET NUMBER:
                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: C1, MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Wi
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US-08-520-678A-29/c

Sequence 29, Application US/08520678A

Sequence 29, Application US/08520678A

Sequence 29, Application US/08520678A

Sequence 29, Application US/08520678A

Sequence 20, Application US/08520678A

APPLICANT: Rice, Charles M.

APPLICANT: Rolykhalov, Alexander A.

APPLICANT: Rolykhalov, Alexander A.

TITLE OF INVENTION: O'IRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

TITLE OF INVENTION: O'IRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.

STREET: 7733 Forsyth Blvd., Suite 1400

CITY: St. Louis

STREET: MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 AAATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCAT 154
                                                                                               Gaps
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45; Indels
                                                                                                                                                    96 AATGACTACATTTGAAAGAAAACTTCAAGATCAAGATAAGAAA 138
                                                                                                                                                                                                  ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%; Score 30.8; DB 2;
53.3%; Pred. No. 3.6;
cive 0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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Steven Steven C. Barash
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
Michael R. Fannon
STREET: 9410 Key West Avenue
STREET: 9410 Key West Avenue
STATE: Maryland
COUNTRY: Maryland
COUNTRY: Fackville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 CTACATTTGAAAGAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 crattacticada a cancidencia cha con contra cara cana con contra con contra con contra con contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-CCt-1997 CLASSIFICATION: cURROWN>PRIOR APPLICATION SAPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.6%; Score 30.8; DB 4; Best Local Similarity 51.4%; Pred. No. 4.3; Matches 71; Conservative 0; Mismatches 67;
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FILING DATE: January 5, 1996
APPLICATION UNMERS: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
TELECOMMUNICATION INFORMATION:
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Sequence 4397, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (240) 314-122
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INFORMATION FOR SEQ ID NO: 4397
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: OVARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1. 6297003
Patent No. 6297003
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: ROLVKhalov, Alexander A.
APPLICANT: ROLVKhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: E. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 ANATGACTACATTIGAAAGAAACTICAAGAICAAGATAAGAAAAGCCAAGAAGTITCAT 154
     DB 3; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
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53.3%; Pred. No. 3.6;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CONTWARE: Patentin Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party Party P
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RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/08897126
Patent No. 6297003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029
TELEPHONE: 314-727-5188
TELEPHONE: 314-727-5188
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TYPE: nucleic acid
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MEDIUM TYPE: Floppy
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Matches 65; Conserv
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US-08-956-171E-4397
                                                                                                                                                                                                                                                                    CC 95
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patent No. 6617109

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patent Stolk, John A.

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Best Local Similarity 51.2%; Pred. No. 4.4;
Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.6%; Score 30.8; Di Best Local Similarity 51.2%; Pred. No. 4.4; Matches 65; Conservative 0; Mismatches
TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 210121.484C2
CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FASESEQ for Windows Version 3.0
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LOCATION: (1)...(396)

OTHER INFORMATION: n = A,T,C or G

US-09-713-550-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KBY: misc_feature
loCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-640-173-16
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CCAAGAA 147
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                                                                                                                                                                                                                                                               SEQ ID NO 16
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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Sequence 22, Application US/08897126
Patent No. 6297003
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: ROLPHALOV. Alexander A.
APPLICANT: ROLPHALOV. Alexander A.
TILE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF NUMBER OF SEQUENCE. 3 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Howell & Haferkamp, L.C.
                                                                 APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 AAAGAAGCCCCAAAGAAAGCAAACCCCAGATGAGGAAAGGAAAACGGCAGGAAATGACTACATT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 TGAAAGAAAACTTCAAGATCAAGATAAGAAAAGCCAAGAAGTTTCATCCACTTCTAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 AAAACAGGAAATGGCCTAAGAGGCCGGAGTGTTTACCCCAACCTTCAT 84
                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/520,678A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                 ...ukeSSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.4;
Pred. No. 5.
Sequence 22, Application US/08520678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Henderson, Melodie W. REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
US-08-520-678A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.8%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                STATE: MO
COUNTRY: US
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-897-126-22/c
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7733 Forsyth Blvd., Suite 1400

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CONPUTER: BADABLE PORM:

COMPUTER: READABLE PORM:

MEDIUM TYPER RADABLE PORM:

COMPUTER: RIANGE FLODG/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: RIANGE FLODG/MS-DOS

OFFICATION NUMBER: US/08/897,126

FLIANG DATE:

CLASSITEATION DATE:

APPLICATION NUMBER: 08/520,678

FLIANG DATE:

ATOMNER: Henderson, Melodie W.

RESTRANCE/COCKET NUMBER: 03-639-6336

TELEKX: 314-727-692

TELEKX: 314-727-692

TELEKX: 314-727-693

TELEKX: 314-727-693

TELEX: SOCIE 30.4; DB 3; Length 356;

MORGIN: 356 base pairs

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